



wwPDB EM Validation Summary Report ⓘ

Jun 19, 2026 – 01:56 am BST

PDB ID : 9GMO / pdb_00009gmo
EMDB ID : EMD-51452
Title : eIF6-bound pre-60S large ribosomal subunit incorporating mutant uL16
Authors : Bothe, A.; Ban, N.; Kostova, K.
Deposited on : 2024-08-29
Resolution : 2.59 Å(reported)
Based on initial model : 8a3d

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

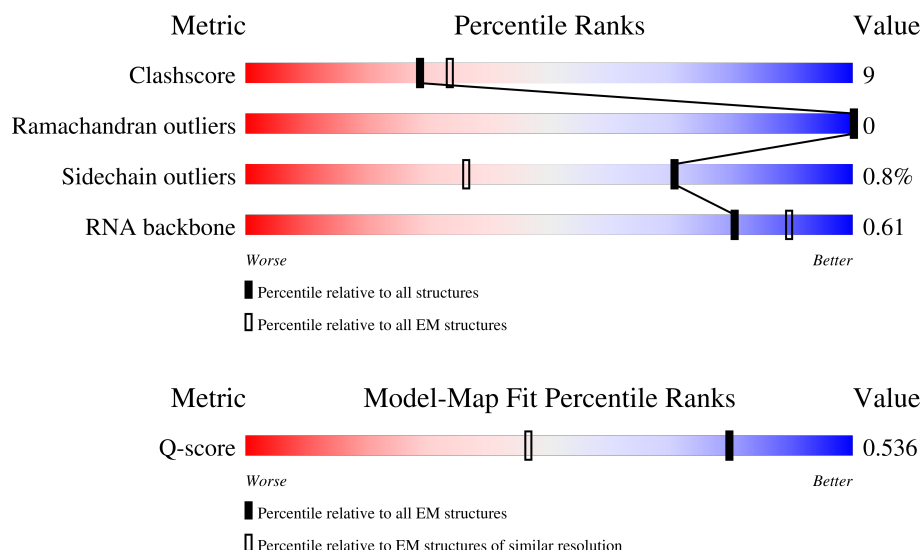
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.59 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



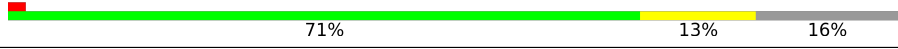
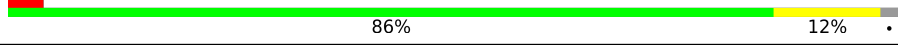
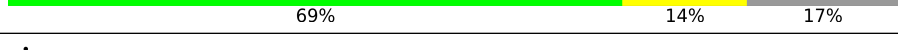
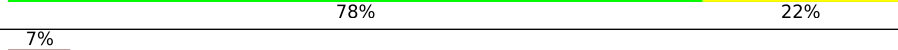
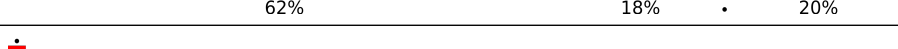
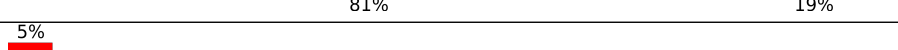
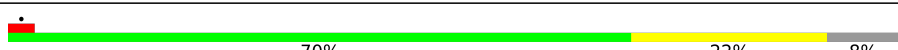
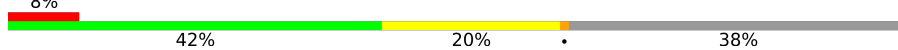
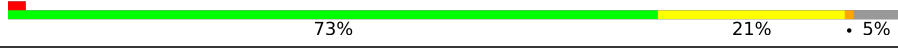
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7741 (2.09 - 3.09)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	5064	
2	B	119	
3	C	157	

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Mol	Chain	Length	Quality of chain
4	D	257	
5	E	403	
6	F	427	
7	G	297	
8	H	288	
9	I	203	
10	J	184	
11	K	188	
12	L	196	
13	M	176	
14	N	160	
15	O	128	
16	P	140	
17	Q	157	
18	R	156	
19	S	145	
20	T	136	
21	U	148	
22	V	159	
23	W	115	
24	X	125	
25	Y	135	
26	Z	110	
27	a	117	
28	b	123	

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Mol	Chain	Length	Quality of chain
29	c	105	
30	d	97	
31	e	70	
32	f	51	
33	g	128	
34	h	245	
35	i	106	
36	j	92	
37	k	137	
38	l	204	
39	m	248	
40	n	266	
41	o	192	
42	p	204	
43	q	178	
44	r	211	
45	s	215	
46	0	477	

2 Entry composition [i](#)

There are 53 unique types of molecules in this entry. The entry contains 132746 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3394	Total	C	N	O	P	1	0
			72870	32489	13334	23652	3395		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	118	Total	C	N	O	P	0	0
			2518	1122	449	829	118		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	148	Total	C	N	O	P	0	0
			3156	1408	563	1037	148		

- Molecule 4 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	246	Total	C	N	O	S	0	0
			1887	1183	387	311	6		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	395	Total	C	N	O	S	1	0
			3194	2034	600	545	15		

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	360	Total	C	N	O	S	0	0
			2860	1800	572	475	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	292	Total	C	N	O	S	0	0
			2372	1503	431	424	14		

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	218	Total	C	N	O	S	0	0
			1752	1128	333	287	4		

- Molecule 9 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 10 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 11 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 12 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	157	Total	C	N	O	S	0	0
			1304	813	280	202	9		

- Molecule 13 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	176	Total	C	N	O	S	0	0
			1461	930	284	236	11		

- Molecule 14 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 15 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	99	Total	C	N	O	S	0	0
			804	516	140	146	2		

- Molecule 16 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	132	Total	C	N	O	S	0	0
			985	621	185	174	5		

- Molecule 17 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	62	Total	C	N	O	S	0	0
			519	332	101	83	3		

- Molecule 18 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 19 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 20 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 21 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 22 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	99	Total	C	N	O	S	0	0
			806	500	177	125	4		

- Molecule 23 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	100	Total	C	N	O	S	0	0
			772	490	136	139	7		

- Molecule 24 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	106	Total	C	N	O	S	0	0
			868	551	170	145	2		

- Molecule 25 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 26 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	109	Total	C	N	O	S	1	0
			879	557	174	144	4		

- Molecule 27 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	111	Total	C	N	O	S	0	0
			882	552	182	142	6		

- Molecule 28 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 29 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 30 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	86	Total	C	N	O	S	1	0
			713	442	155	111	5		

- Molecule 31 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 32 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 33 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 34 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	225	Total	C	N	O	S	0	0
			1712	1065	295	340	12		

- Molecule 35 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 36 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	92	Total	C	N	O	S	0	0
			716	450	137	121	8		

- Molecule 37 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	124	Total	C	N	O	S	0	0
			992	615	206	167	4		

- Molecule 38 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	203	Total	C	N	O	S	1	0
			1708	1077	360	267	4		

- Molecule 39 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	224	Total	C	N	O	S	0	0
			1856	1192	356	299	9		

- Molecule 40 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	223	Total	C	N	O	S	0	0
			1809	1153	349	303	4		

- Molecule 41 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 42 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	203	Total	C	N	O	S	0	0
			1647	1045	318	272	12		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
p	?	-	MET	deletion	UNP P27635
p	?	-	LEU	deletion	UNP P27635
p	?	-	SER	deletion	UNP P27635
p	?	-	CYS	deletion	UNP P27635
p	?	-	ALA	deletion	UNP P27635
p	?	-	GLY	deletion	UNP P27635
p	?	-	ALA	deletion	UNP P27635
p	?	-	ASP	deletion	UNP P27635
p	?	-	ARG	deletion	UNP P27635
p	?	-	LEU	deletion	UNP P27635

- Molecule 43 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	170	Total	C	N	O	S	0	0
			1358	858	253	241	6		

- Molecule 44 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	206	Total	C	N	O	S	0	0
			1664	1041	345	274	4		

- Molecule 45 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 46 is a protein called Cytoplasmic 60S subunit biogenesis factor ZNF622.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	0	43	Total	C	N	O	S	0	0
			363	226	72	59	6		

- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
47	A	213	Total 213	Mg 213	0
47	B	3	Total 3	Mg 3	0
47	C	6	Total 6	Mg 6	0
47	L	1	Total 1	Mg 1	0
47	P	1	Total 1	Mg 1	0
47	U	1	Total 1	Mg 1	0
47	i	1	Total 1	Mg 1	0
47	p	1	Total 1	Mg 1	0

- Molecule 48 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
48	A	139	Total 139	K 139	0
48	B	1	Total 1	K 1	0
48	D	3	Total 3	K 3	0
48	F	1	Total 1	K 1	0
48	J	1	Total 1	K 1	0
48	N	1	Total 1	K 1	0
48	V	1	Total 1	K 1	0
48	Y	1	Total 1	K 1	0
48	Z	1	Total 1	K 1	0
48	f	1	Total 1	K 1	0
48	i	1	Total 1	K 1	0
48	l	2	Total 2	K 2	0

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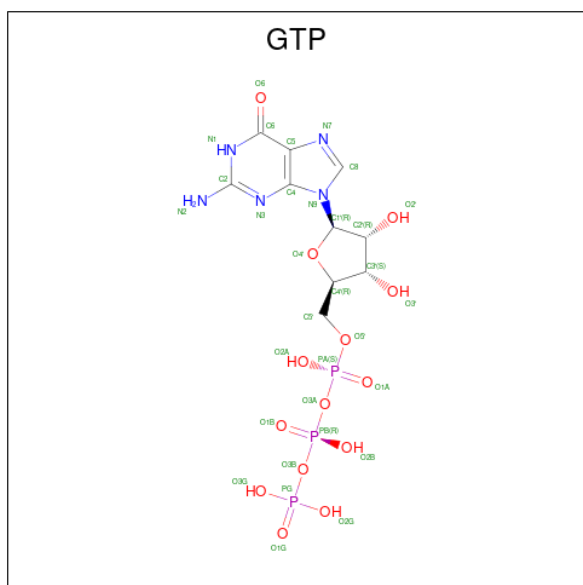
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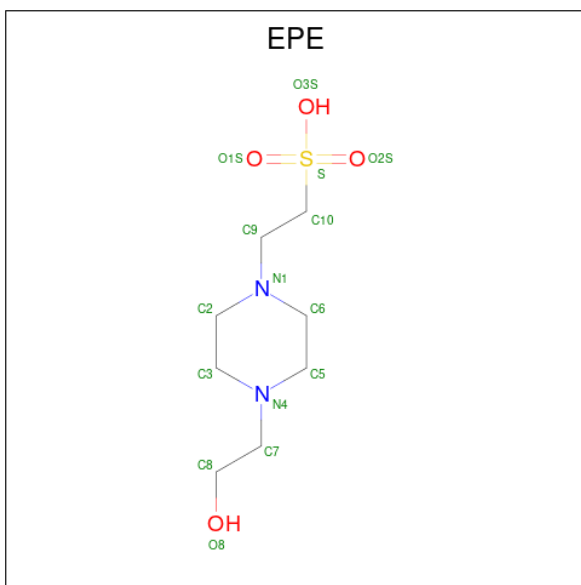
Mol	Chain	Residues	Atoms		AltConf
48	o	1	Total	K	0
			1	1	
48	p	1	Total	K	0
			1	1	

- Molecule 49 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
49	A	2	Total	Na	0
			2	2	

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).





Mol	Chain	Residues	Atoms					AltConf
51	M	1	Total	C	N	O	S	0
			15	8	2	4	1	

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	a	1	Total	Zn	0
			1	1	
52	d	1	Total	Zn	0
			1	1	
52	g	1	Total	Zn	0
			1	1	
52	i	1	Total	Zn	0
			1	1	
52	j	1	Total	Zn	0
			1	1	

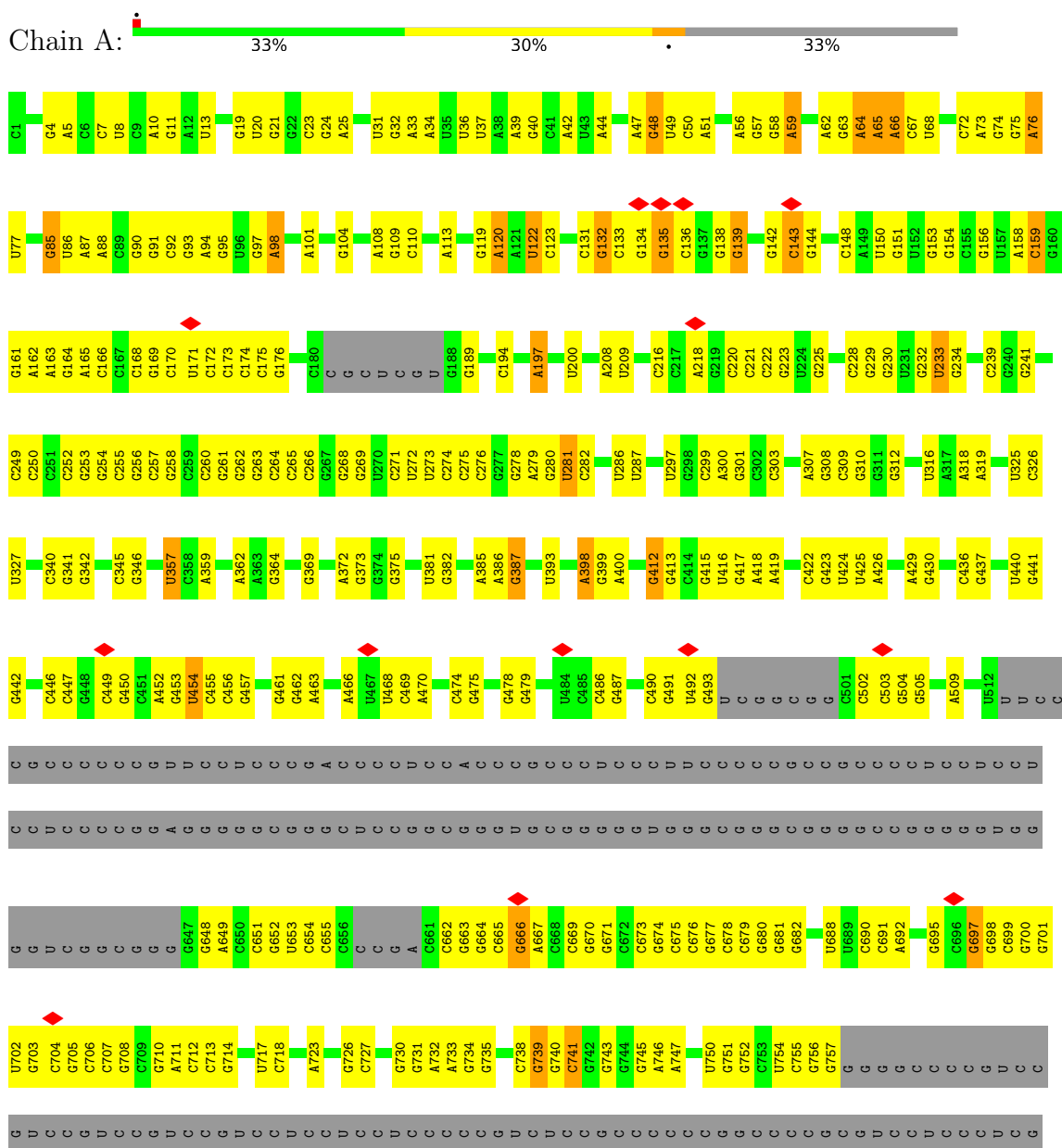
- Molecule 53 is water.

Mol	Chain	Residues	Atoms		AltConf
53	A	4	Total	O	0
			4	4	
53	G	1	Total	O	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

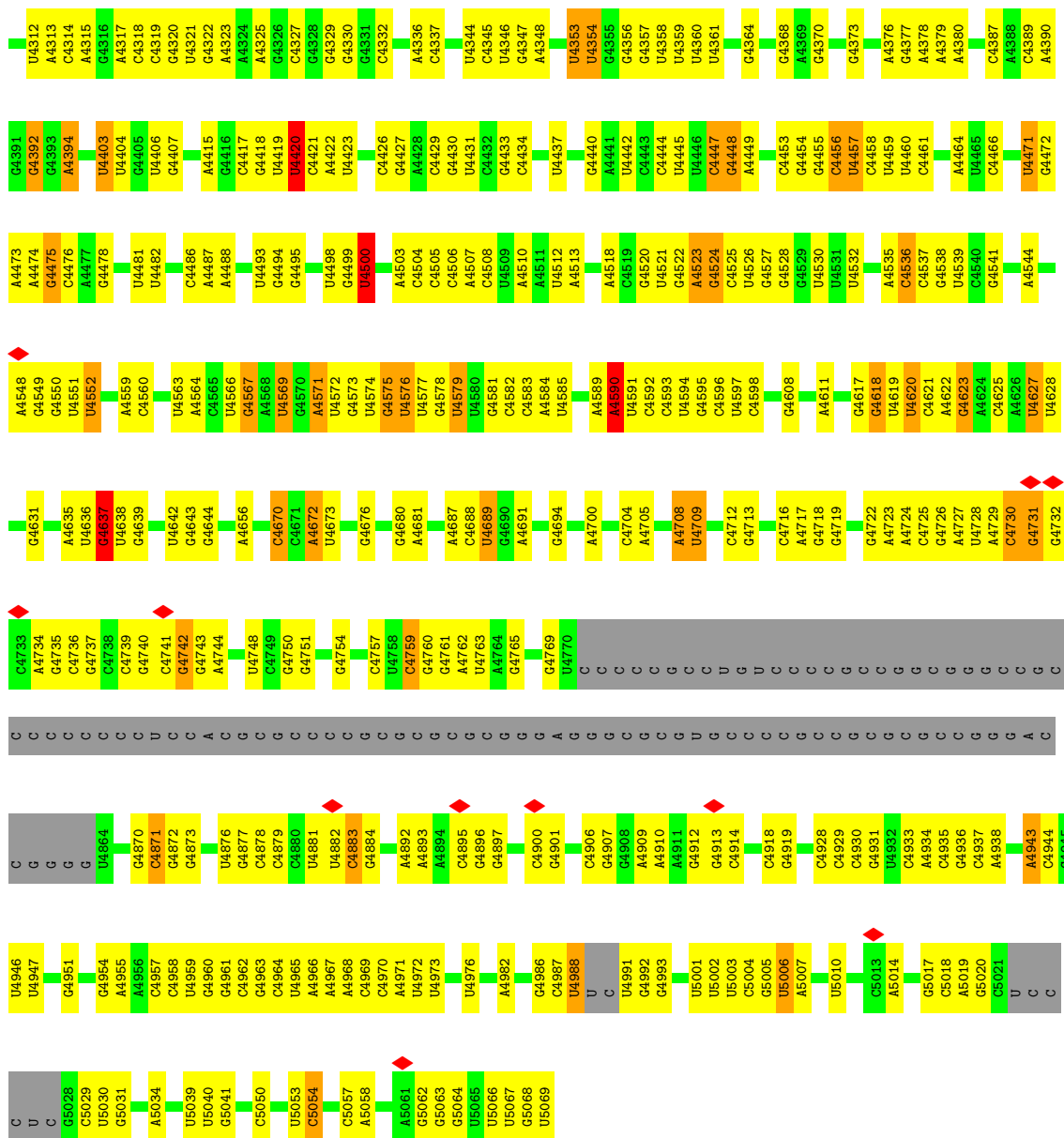
• Molecule 1: 28S rRNA





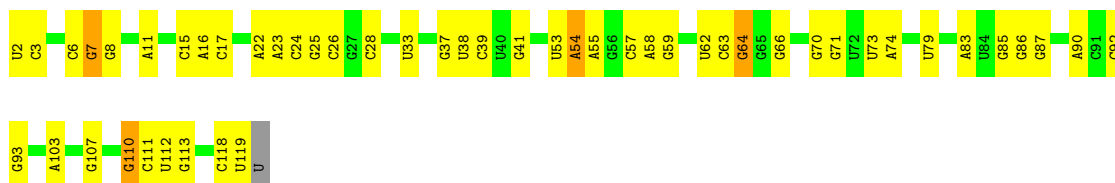


G4228	G4150	C4080	G	PSU	G3888	A3816	U3724	G3661	C	U	C
U4229	G4151	G4081	U	A	C3893	A3817	G3735	A3662	G	C	G
A4233	G4152	G4084	C	G	A3894	U13818	G3743	A3663	C	C	C
A4234	C4153	G4084	A	A	A3894	G3819	G3744	G3664	C	C	C
G4237	C4154	C4088	G	A	C3895	G3820	U3745	G3665	U	C	C
G4238	C4155	C4089	C	U	C3896	G3823	A3748	C3666	A	C	C
A4239	C4156	G4090	C	A	G3897	A3824	A3748	C3667	G	C	C
G4240	A4158	G4093	G	A	C3898	A3825	A3748	C3668	C3598	C	C
G4246	C4159	G	G	G	G3899	C3826	G3753	C3669	A3599	C	C
G4247	C4160	G4093	U	U	G3900	G3827	G3754	C3670	C3600	C	C
A4251	G4161	G	C	G	A3901	A3828	G3754	C3671	C	C	C
A4252	C4162	G	C	G	G3905	G3829	G3757	C3672	G3603	G	C
A4253	C4165	G	U	A	A3906	G3830	G3757	C3673	A3604	C	C
A4254	G4168	A	G	G	A3907	U3831	PSU	G3681	C3605	G	C
A4255	C4169	G	G	A	G3908	U3831	A	A3682	U3607	C	C
A4260	C4170	C	C	C	C3909	C3835	A2M	C3683	C3608	C	C
C4261	A4171	C	G	C	C3910	A3836	PSU	G3684	A3609	C	C
C4262	C4172	C	C	C	C3911	C3837	A	C3685	A3610	C	C
C4263	A4173	C	C	C	U3912	U3838	PSU	G3686	A3611	C	C
C4264	C4174	G	C	C	U3915	G3839	G	C3687	C3612	C	C
U4265	C4175	G	G	C	G3916	U3840	A	U3688	G3613	C	C
G4266	C4176	G	C	C	A3917	C3843	C3767	C3689	G3614	C	C
G4267	C4177	G	C	C	G3918	U3844	U3768	A3692	G3615	C	C
A4268	C4178	G	U	C	C3919	C3844	U3769	G3697	U3616	C	C
A4272	C4179	U	C	C	U3920	U3848	U3770	U3695	G3617	C	C
A4273	U4188	C	C	C	A3923	A3849	C3771	C3696	C3618	C	C
G4275	U4189	C	C	C	C3924	C3850	U3772	C3697	C3619	C	C
G4277	U4190	U	C	C	U3925	U3851	U3773	U3698	C3620	C	C
A4281	A4191	C	A	C	C3926	A3852	A3774	C3699	A3621	C	C
A4282	A4192	G	U	C	U3927	U3853	A3775	C3700	C3622	C	C
U4285	C4196	C	C	C	A3928	C3854	G3776	C3701	C3623	C	C
C4286	C4197	C	C	C	U3927	C3855	G3777	A3624	G3625	C	C
C4287	C4198	G	C	C	A3928	A3856	U3778	C3702	G3626	C	C
G4291	C4199	C	U	C	U3932	A3861	C3782	U3707	G3627	C	C
A4292	A4203	C	A	C	G3933	A3862	A3783	C3708	G3628	C	C
A4293	U4208	C	U	C	G3934	A3862	A3784	U3709	C3629	C	C
U4296	G4209	C	C	C	C3937	A3865	U3785	G3710	G3634	C	C
G4297	A4212	C	C	C	U3940	C3866	U3786	A3711	A3635	C	C
A4298	A4213	C	C	C	G3941	A3867	G3787	A3712	C3636	C	C
U4300	A4214	C	C	C	A3942	C3868	C3788	U3713	U3637	C	C
U4301	C4219	C	C	C	A3943	C3869	C3789	G3714	G3638	C	C
U4302	A4220	C	C	C	A3944	C3870	U3790	C3715	U3639	C	C
A4303	C4225	C	C	C	G3945	A3871	C3791	C3716	U3640	C	C
A4304	G4226	C	C	C	A3946	A3872	U3793	U3641	U3641	C	C
G4305	U4227	C	C	C	C3947	G3873	C3794	A3717	A3642	C	C
U4306	C4145	C	C	C	C3948	G3874	A3795	A3718	C	C	C
A4307	G4146	C	C	C	U3948	A3877	A3799	A3719	A3646	C	C
	G4147	C	C	C	A	C3878	A3799	A3723	A3647	C	C
	C4148	C	C	C	U	G3879	A3799	A3724	A3648	C	C
	U4227	C	C	C	G	G3880	C3808	G3725	A3648	C	C
		C	C	C	A	G3881	C3809	A3726	A3653	C	C
		C	C	C	A	C3882	C3810	A3727	A3653	C	C
		C	C	C	G	U3883	C3811	U3728	A3656	C	C
		C	C	C	G	U3884	C3812	U3729	U3657	C	C
		C	C	C	U	C3887	C3813	C3731	C3658	C	C
		C	C	C	G		U3814	A3732	G3659	C	C
		C	C	C	G		G3815	A3733	C3660	C	C



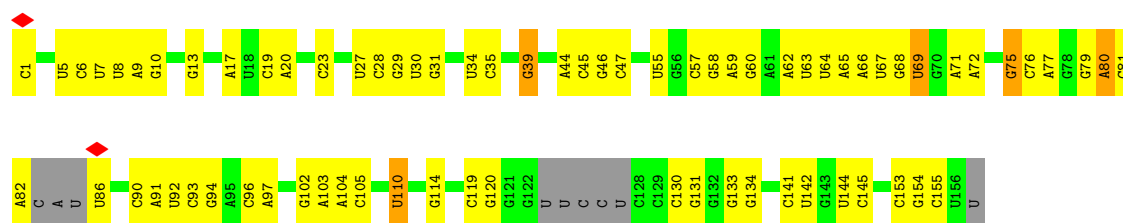
• Molecule 2: 5S rRNA

Chain B: 57% 39%

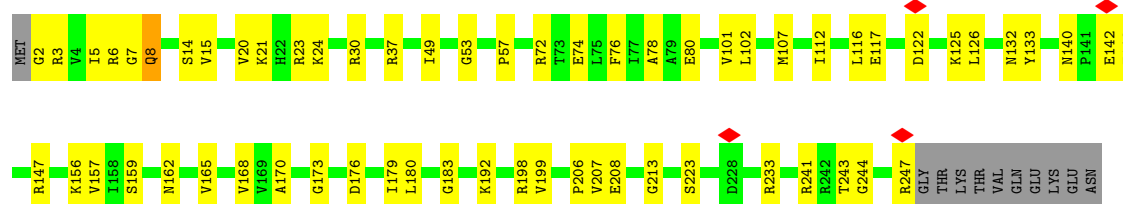


• Molecule 3: 5.8S rRNA

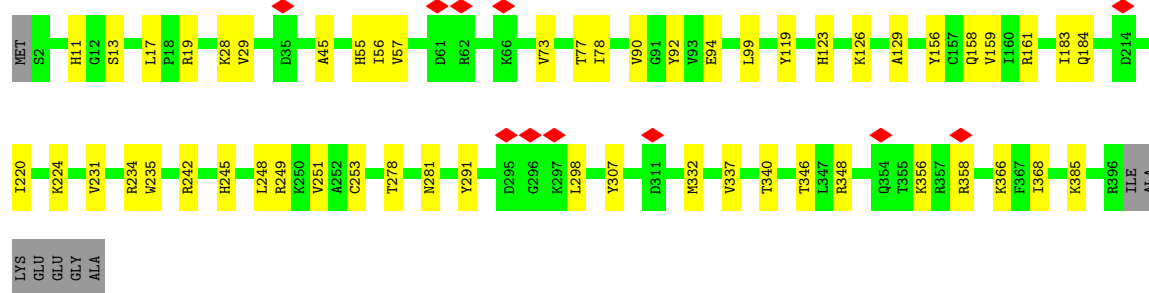
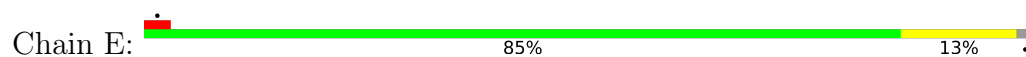
Chain C: 48% 43% 6%



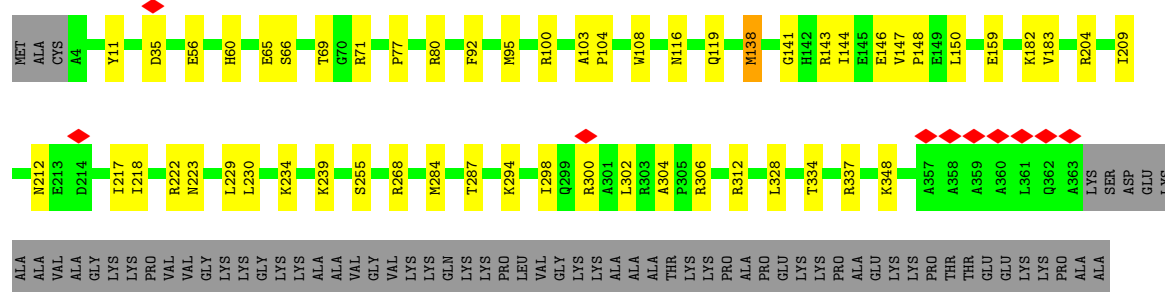
• Molecule 4: 60S ribosomal protein L8



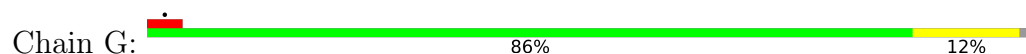
• Molecule 5: 60S ribosomal protein L3



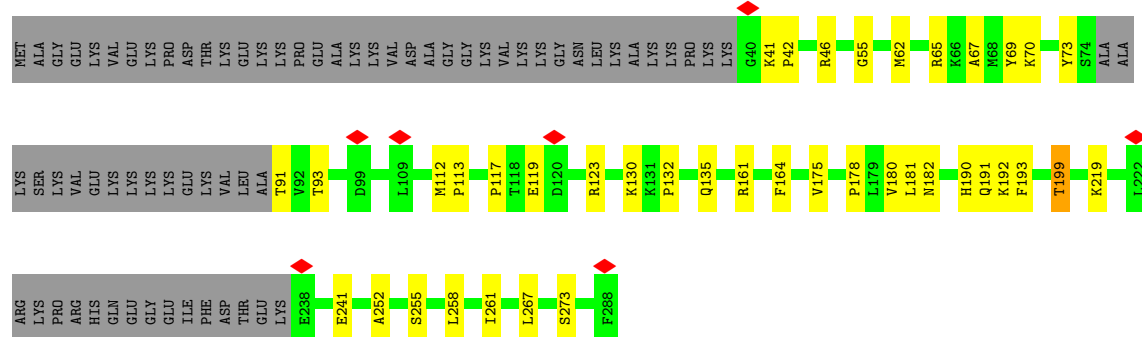
• Molecule 6: 60S ribosomal protein L4



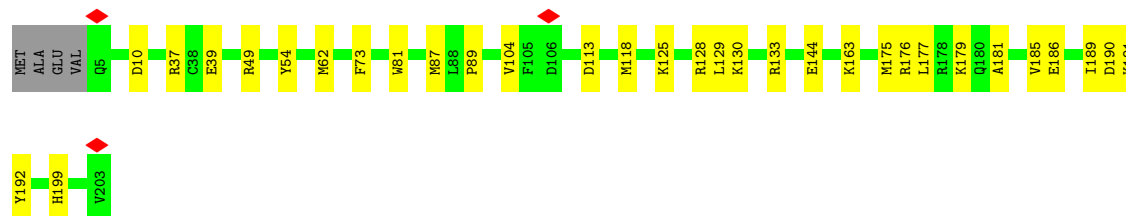
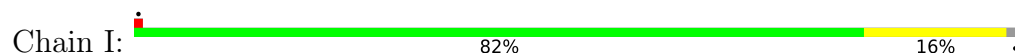
• Molecule 7: 60S ribosomal protein L5



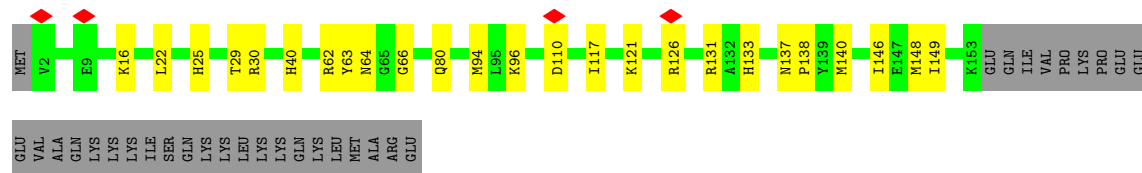
- Molecule 8: Large ribosomal subunit protein eL6



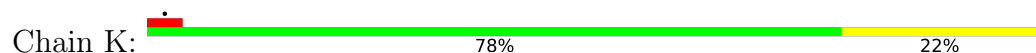
- Molecule 9: 60S ribosomal protein L13a

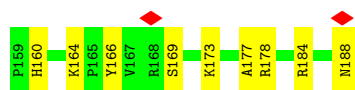


- Molecule 10: 60S ribosomal protein L17

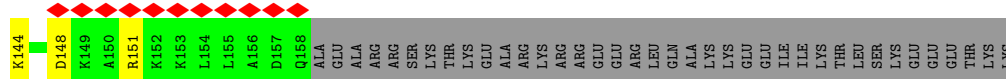
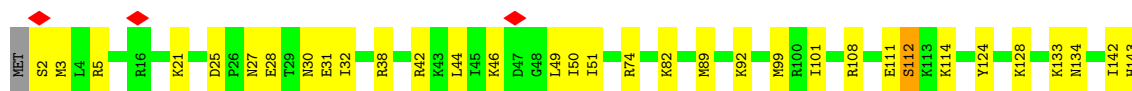


- Molecule 11: 60S ribosomal protein L18

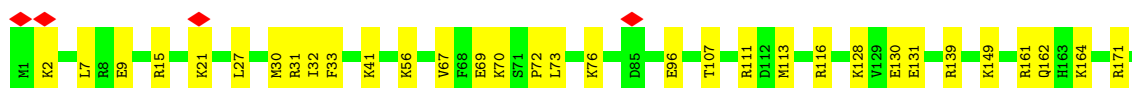
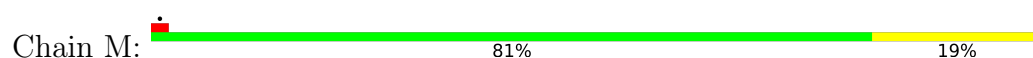




- Molecule 12: 60S ribosomal protein L19



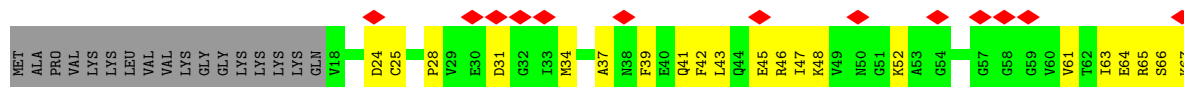
- Molecule 13: 60S ribosomal protein L18a



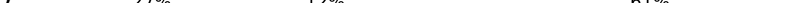
- Molecule 14: 60S ribosomal protein L21

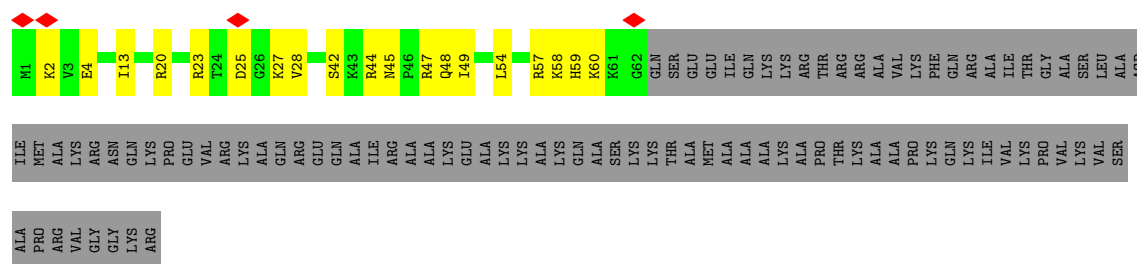


- Molecule 15: 60S ribosomal protein L22

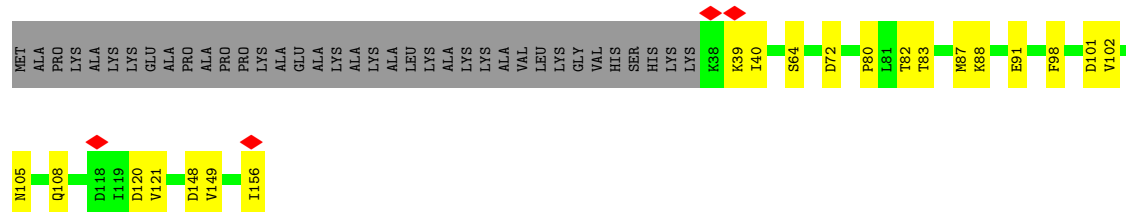


- Molecule 16: 60S ribosomal protein L23

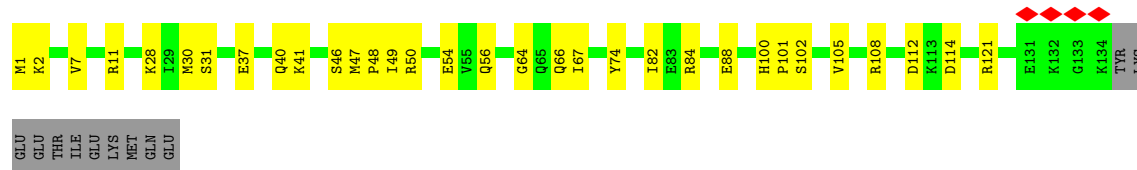
- Chain Q: 

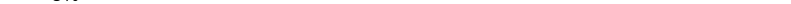


- Chain R: 63% 13% 24%



- Chain S: 70% 22% 8%

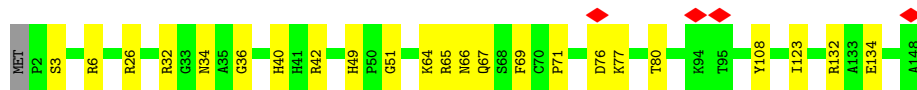
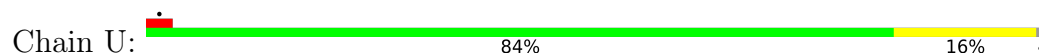


- Chain T:  8% 69% 29%

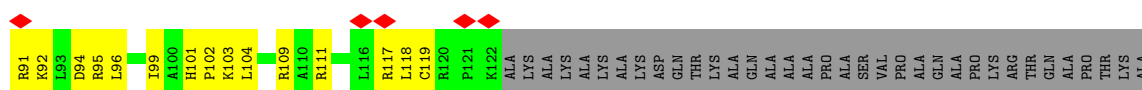
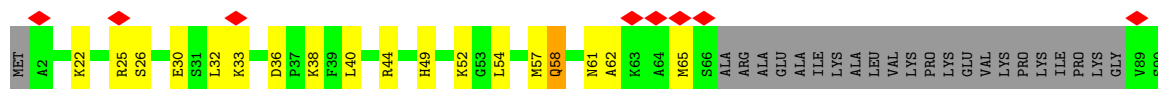




- Molecule 21: 60S ribosomal protein L27a



- Molecule 22: 60S ribosomal protein L29



- Molecule 23: 60S ribosomal protein L30



- Molecule 24: 60S ribosomal protein L31



- Molecule 25: 60S ribosomal protein L32



GLU
ASN
GLU

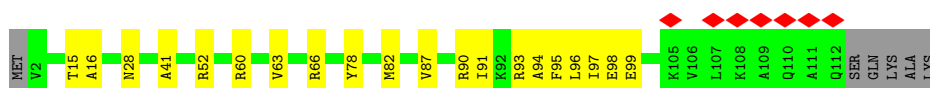
- Molecule 26: 60S ribosomal protein L35a

Chain Z:  83% 16% .



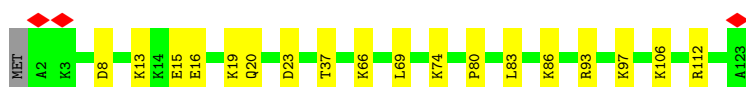
- Molecule 27: 60S ribosomal protein L34

Chain a:  6% 78% 17% 5%



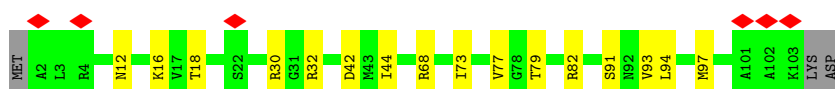
- Molecule 28: 60S ribosomal protein L35

Chain b:  85% 15% .



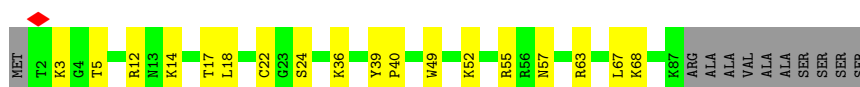
- Molecule 29: 60S ribosomal protein L36

Chain c:  6% 82% 15% .



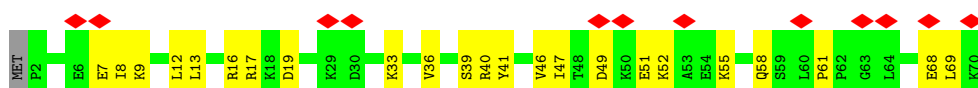
- Molecule 30: 60S ribosomal protein L37

Chain d:  70% 19% 11%



- Molecule 31: 60S ribosomal protein L38

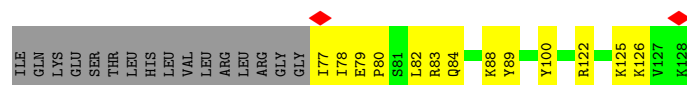
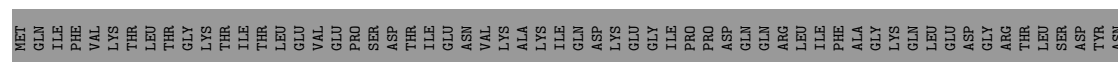
Chain e:  17% 66% 33%



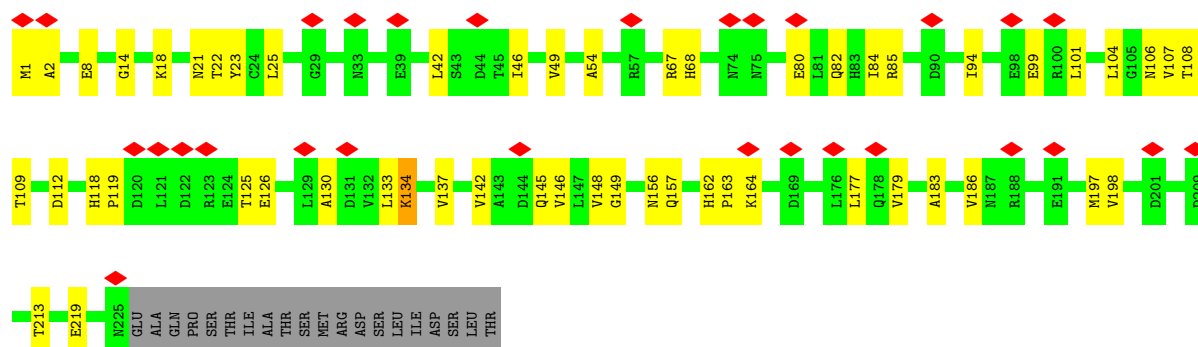
- Molecule 32: 60S ribosomal protein L39



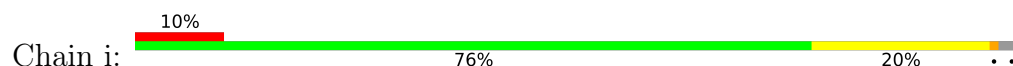
- Molecule 33: Ubiquitin-60S ribosomal protein L40



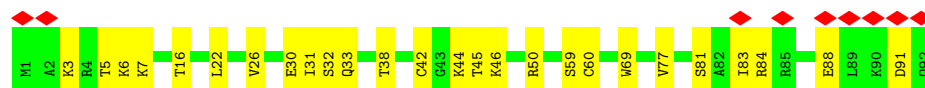
- Molecule 34: Eukaryotic translation initiation factor 6



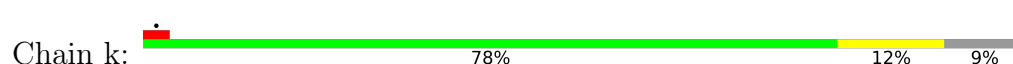
- Molecule 35: 60S ribosomal protein L36a



- Molecule 36: 60S ribosomal protein L37a



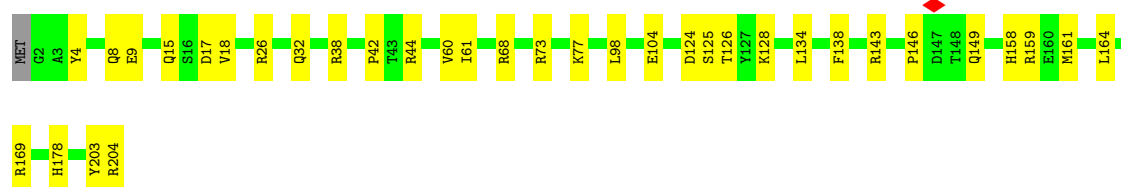
- Molecule 37: 60S ribosomal protein L28





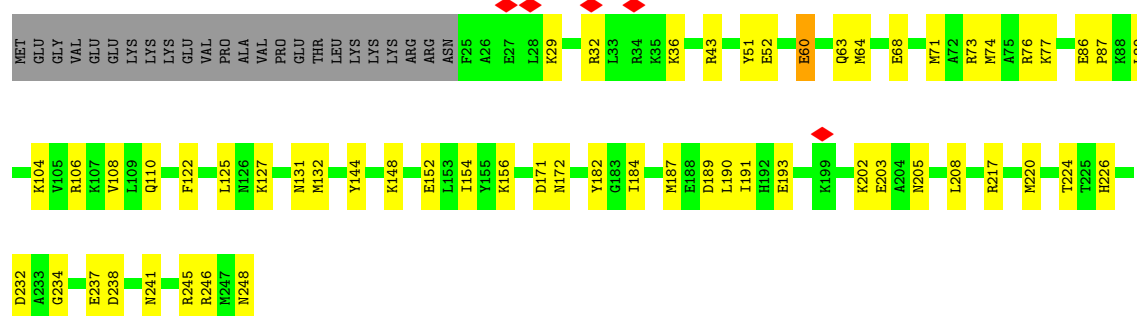
- Molecule 38: 60S ribosomal protein L15

Chain l: 82% 17%



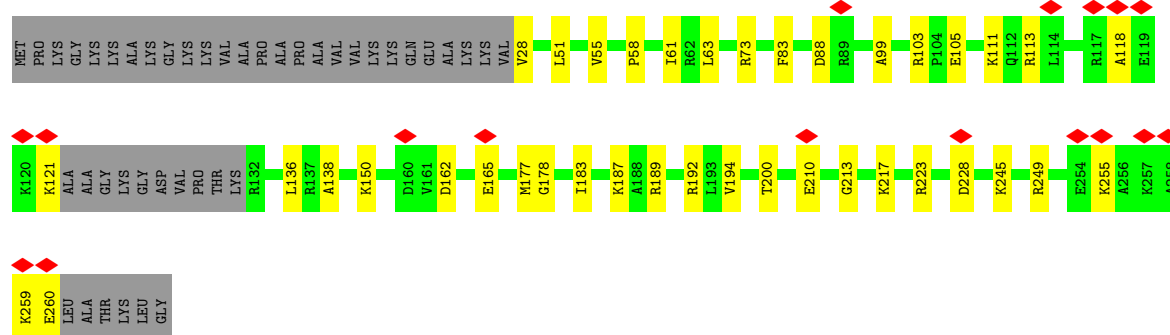
- Molecule 39: Large ribosomal subunit protein uL30

Chain m: 67% 23% 10%



- Molecule 40: 60S ribosomal protein L7a

Chain n: 6% 69% 15% 16%



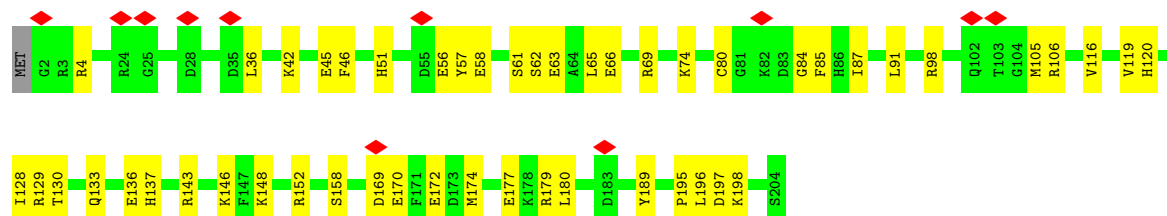
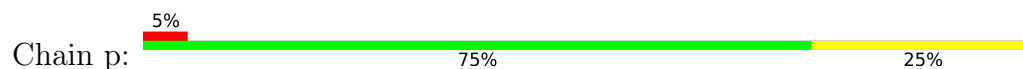
- Molecule 41: 60S ribosomal protein L9

Chain o: 6% 77% 22%

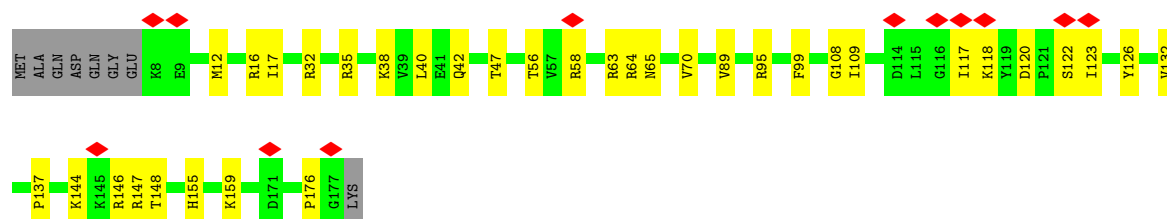
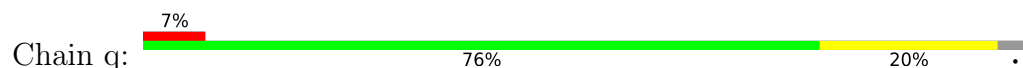




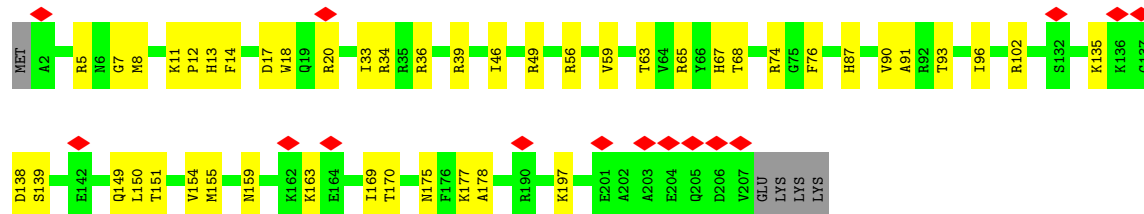
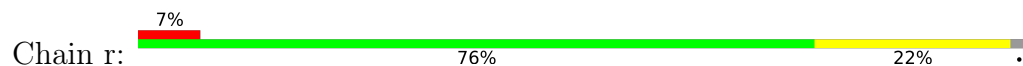
- Molecule 42: Large ribosomal subunit protein uL16



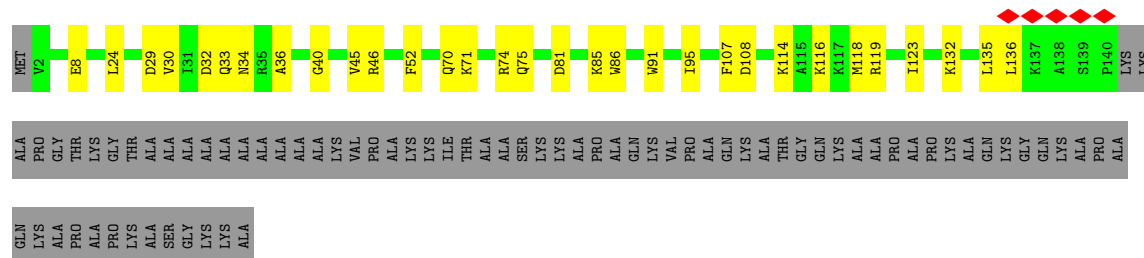
- Molecule 43: 60S ribosomal protein L11



- Molecule 44: 60S ribosomal protein L13



- Molecule 45: 60S ribosomal protein L14



Chain 0: 91%

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.487	Depositor
Minimum map value	-0.586	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	593.6, 593.6, 593.6	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: OMC, K, OMG, ZN, 5MC, 6MZ, UR3, NA, GTP, EPE, A2M, OMU, PSU, UY1, 1MA, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.12	4/78643 (0.0%)	0.21	0/122654
2	B	0.08	0/2813	0.19	0/4384
3	C	0.08	0/3453	0.20	0/5376
4	D	0.10	0/1925	0.28	0/2581
5	E	0.08	0/3265	0.22	0/4369
6	F	0.09	0/2914	0.24	0/3915
7	G	0.08	0/2418	0.24	0/3239
8	H	0.11	0/1786	0.28	0/2395
9	I	0.12	0/1666	0.33	0/2228
10	J	0.12	0/1259	0.36	0/1689
11	K	0.11	0/1537	0.27	0/2052
12	L	0.13	0/1320	0.40	0/1749
13	M	0.11	0/1501	0.30	0/2013
14	N	0.16	0/1326	0.43	0/1770
15	O	0.22	0/818	0.61	0/1098
16	P	0.11	0/999	0.32	0/1340
17	Q	0.17	0/532	0.47	0/708
18	R	0.12	0/993	0.32	0/1334
19	S	0.13	0/1132	0.34	0/1504
20	T	0.12	0/1130	0.35	0/1507
21	U	0.09	0/1191	0.26	0/1591
22	V	0.15	0/819	0.42	0/1081
23	W	0.19	0/783	0.51	0/1052
24	X	0.12	0/883	0.31	0/1190
25	Y	0.11	0/1071	0.31	0/1429
26	Z	0.10	0/901	0.26	0/1206
27	a	0.09	0/892	0.23	0/1189
28	b	0.13	0/1023	0.39	0/1351
29	c	0.13	0/843	0.37	0/1115
30	d	0.07	0/732	0.22	0/968
31	e	0.15	0/575	0.42	0/761
32	f	0.12	0/454	0.30	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	g	0.11	0/435	0.34	0/575
34	h	0.13	0/1736	0.36	0/2362
35	i	0.11	0/855	0.35	0/1128
36	j	0.10	0/726	0.35	0/963
37	k	0.08	0/1007	0.24	0/1351
38	l	0.08	0/1753	0.21	0/2348
39	m	0.11	0/1890	0.28	0/2519
40	n	0.09	0/1840	0.23	0/2476
41	o	0.16	0/1537	0.40	0/2066
42	p	0.13	0/1686	0.35	0/2252
43	q	0.10	0/1381	0.30	0/1848
44	r	0.10	0/1695	0.27	0/2270
45	s	0.12	0/1161	0.36	0/1554
46	0	0.08	0/368	0.26	0/484
All	All	0.12	4/139667 (0.0%)	0.25	0/205633

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4523	A2M	O3'-P	5.06	1.61	1.56
1	A	3785	A2M	O3'-P	5.03	1.61	1.56
1	A	398	A2M	O3'-P	5.02	1.61	1.56
1	A	3718	A2M	O3'-P	5.00	1.61	1.56

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	72870	0	36883	1229	0
2	B	2518	0	1273	40	0
3	C	3156	0	1602	56	0
4	D	1887	0	1983	47	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	3194	0	3335	41	0
6	F	2860	0	3026	50	0
7	G	2372	0	2403	30	0
8	H	1752	0	1904	28	0
9	I	1634	0	1779	23	0
10	J	1233	0	1263	19	0
11	K	1513	0	1628	38	0
12	L	1304	0	1433	30	0
13	M	1461	0	1502	26	0
14	N	1298	0	1366	37	0
15	O	804	0	825	28	0
16	P	985	0	1044	27	0
17	Q	519	0	533	17	0
18	R	976	0	1053	15	0
19	S	1115	0	1205	28	0
20	T	1107	0	1182	32	0
21	U	1162	0	1213	19	0
22	V	806	0	865	26	0
23	W	772	0	808	34	0
24	X	868	0	912	11	0
25	Y	1053	0	1147	22	0
26	Z	879	0	915	13	0
27	a	882	0	972	14	0
28	b	1015	0	1148	19	0
29	c	832	0	917	11	0
30	d	713	0	746	15	0
31	e	569	0	637	19	0
32	f	444	0	482	12	0
33	g	429	0	465	13	0
34	h	1712	0	1689	40	0
35	i	842	0	912	15	0
36	j	716	0	768	22	0
37	k	992	0	1052	12	0
38	l	1708	0	1757	28	0
39	m	1856	0	1983	47	0
40	n	1809	0	1941	28	0
41	o	1518	0	1600	34	0
42	p	1647	0	1694	39	0
43	q	1358	0	1388	24	0
44	r	1664	0	1773	35	0
45	s	1138	0	1204	21	0
46	0	363	0	377	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	A	213	0	0	0	0
47	B	3	0	0	0	0
47	C	6	0	0	0	0
47	L	1	0	0	0	0
47	P	1	0	0	0	0
47	U	1	0	0	0	0
47	i	1	0	0	0	0
47	p	1	0	0	0	0
48	A	139	0	0	0	0
48	B	1	0	0	0	0
48	D	3	0	0	0	0
48	F	1	0	0	0	0
48	J	1	0	0	0	0
48	N	1	0	0	0	0
48	V	1	0	0	0	0
48	Y	1	0	0	0	0
48	Z	1	0	0	0	0
48	f	1	0	0	0	0
48	i	1	0	0	0	0
48	l	2	0	0	0	0
48	o	1	0	0	0	0
48	p	1	0	0	0	0
49	A	2	0	0	0	0
50	B	32	0	11	1	0
51	M	15	0	17	1	0
52	a	1	0	0	0	0
52	d	1	0	0	0	0
52	g	1	0	0	0	0
52	i	1	0	0	0	0
52	j	1	0	0	0	0
53	A	4	0	0	0	0
53	G	1	0	0	1	0
All	All	132746	0	96615	2108	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 2108 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2845:A:H61	1:A:3843:C:H42	1.06	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:102:ARG:H	20:T:102:ARG:HE	1.20	0.87
1:A:2845:A:H61	1:A:3843:C:N4	1.75	0.84
1:A:2520:C:O2	1:A:2640:G:N2	2.11	0.84
1:A:3723:A:H2'	1:A:3724:A2M:H8	1.59	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	244/257 (95%)	235 (96%)	9 (4%)	0	100	100
5	E	394/403 (98%)	390 (99%)	4 (1%)	0	100	100
6	F	358/427 (84%)	353 (99%)	5 (1%)	0	100	100
7	G	290/297 (98%)	286 (99%)	4 (1%)	0	100	100
8	H	212/288 (74%)	206 (97%)	6 (3%)	0	100	100
9	I	197/203 (97%)	196 (100%)	1 (0%)	0	100	100
10	J	150/184 (82%)	150 (100%)	0	0	100	100
11	K	185/188 (98%)	183 (99%)	2 (1%)	0	100	100
12	L	155/196 (79%)	154 (99%)	1 (1%)	0	100	100
13	M	174/176 (99%)	170 (98%)	4 (2%)	0	100	100
14	N	157/160 (98%)	156 (99%)	1 (1%)	0	100	100
15	O	97/128 (76%)	92 (95%)	5 (5%)	0	100	100
16	P	130/140 (93%)	129 (99%)	1 (1%)	0	100	100
17	Q	60/157 (38%)	60 (100%)	0	0	100	100
18	R	117/156 (75%)	115 (98%)	2 (2%)	0	100	100
19	S	132/145 (91%)	130 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	133/136 (98%)	130 (98%)	3 (2%)	0	100	100
21	U	145/148 (98%)	144 (99%)	1 (1%)	0	100	100
22	V	95/159 (60%)	94 (99%)	1 (1%)	0	100	100
23	W	98/115 (85%)	98 (100%)	0	0	100	100
24	X	104/125 (83%)	104 (100%)	0	0	100	100
25	Y	126/135 (93%)	126 (100%)	0	0	100	100
26	Z	108/110 (98%)	108 (100%)	0	0	100	100
27	a	109/117 (93%)	108 (99%)	1 (1%)	0	100	100
28	b	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
29	c	100/105 (95%)	100 (100%)	0	0	100	100
30	d	85/97 (88%)	85 (100%)	0	0	100	100
31	e	67/70 (96%)	67 (100%)	0	0	100	100
32	f	48/51 (94%)	48 (100%)	0	0	100	100
33	g	50/128 (39%)	50 (100%)	0	0	100	100
34	h	223/245 (91%)	218 (98%)	5 (2%)	0	100	100
35	i	101/106 (95%)	98 (97%)	3 (3%)	0	100	100
36	j	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
37	k	122/137 (89%)	121 (99%)	1 (1%)	0	100	100
38	l	202/204 (99%)	200 (99%)	2 (1%)	0	100	100
39	m	222/248 (90%)	217 (98%)	5 (2%)	0	100	100
40	n	219/266 (82%)	216 (99%)	3 (1%)	0	100	100
41	o	188/192 (98%)	186 (99%)	2 (1%)	0	100	100
42	p	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
43	q	168/178 (94%)	167 (99%)	1 (1%)	0	100	100
44	r	204/211 (97%)	201 (98%)	3 (2%)	0	100	100
45	s	137/215 (64%)	136 (99%)	1 (1%)	0	100	100
46	0	41/477 (9%)	41 (100%)	0	0	100	100
All	All	6558/7899 (83%)	6472 (99%)	86 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	189/199 (95%)	187 (99%)	2 (1%)	65	84
5	E	345/349 (99%)	345 (100%)	0	100	100
6	F	297/348 (85%)	296 (100%)	1 (0%)	86	94
7	G	245/250 (98%)	244 (100%)	1 (0%)	84	93
8	H	193/252 (77%)	191 (99%)	2 (1%)	68	86
9	I	171/174 (98%)	171 (100%)	0	100	100
10	J	133/163 (82%)	133 (100%)	0	100	100
11	K	164/165 (99%)	164 (100%)	0	100	100
12	L	138/175 (79%)	136 (99%)	2 (1%)	59	81
13	M	157/157 (100%)	155 (99%)	2 (1%)	61	82
14	N	139/140 (99%)	136 (98%)	3 (2%)	45	72
15	O	88/115 (76%)	88 (100%)	0	100	100
16	P	102/107 (95%)	102 (100%)	0	100	100
17	Q	54/126 (43%)	54 (100%)	0	100	100
18	R	107/133 (80%)	107 (100%)	0	100	100
19	S	124/135 (92%)	123 (99%)	1 (1%)	73	88
20	T	117/118 (99%)	113 (97%)	4 (3%)	32	60
21	U	120/121 (99%)	120 (100%)	0	100	100
22	V	82/126 (65%)	81 (99%)	1 (1%)	63	83
23	W	84/97 (87%)	83 (99%)	1 (1%)	63	83
24	X	93/110 (84%)	93 (100%)	0	100	100
25	Y	114/121 (94%)	112 (98%)	2 (2%)	51	76
26	Z	89/89 (100%)	89 (100%)	0	100	100
27	a	95/100 (95%)	93 (98%)	2 (2%)	47	73
28	b	109/110 (99%)	109 (100%)	0	100	100
29	c	86/89 (97%)	84 (98%)	2 (2%)	44	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	d	74/80 (92%)	74 (100%)	0	100	100
31	e	64/65 (98%)	63 (98%)	1 (2%)	55	79
32	f	47/48 (98%)	45 (96%)	2 (4%)	26	51
33	g	48/116 (41%)	48 (100%)	0	100	100
34	h	195/213 (92%)	191 (98%)	4 (2%)	47	73
35	i	91/94 (97%)	88 (97%)	3 (3%)	33	61
36	j	75/75 (100%)	75 (100%)	0	100	100
37	k	107/121 (88%)	107 (100%)	0	100	100
38	l	172/172 (100%)	171 (99%)	1 (1%)	78	91
39	m	192/215 (89%)	191 (100%)	1 (0%)	81	92
40	n	193/223 (86%)	192 (100%)	1 (0%)	81	92
41	o	169/171 (99%)	166 (98%)	3 (2%)	51	76
42	p	173/174 (99%)	173 (100%)	0	100	100
43	q	142/149 (95%)	141 (99%)	1 (1%)	76	89
44	r	172/177 (97%)	170 (99%)	2 (1%)	63	83
45	s	118/161 (73%)	118 (100%)	0	100	100
46	o	38/404 (9%)	37 (97%)	1 (3%)	40	68
All	All	5705/6727 (85%)	5659 (99%)	46 (1%)	70	88

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
32	f	47	THR
35	i	82	MET
34	h	82	GLN
34	h	213	THR
39	m	60	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
28	b	30	GLN
45	s	48	GLN
39	m	63	GLN
45	s	44	GLN

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Mol	Chain	Res	Type
43	q	71	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3366/5064 (66%)	457 (13%)	3 (0%)
2	B	117/119 (98%)	7 (5%)	0
3	C	145/157 (92%)	13 (8%)	0
All	All	3628/5340 (67%)	477 (13%)	3 (0%)

5 of 477 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	13	U
1	A	39	A
1	A	42	A
1	A	47	A
1	A	48	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	486	C
1	A	964	A
1	A	3734	PSU

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

123 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	A	3844	1	18,21,22	1.36	2 (11%)	22,30,33	1.86	3 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	A	4456	1	19,22,23	0.83	0	26,31,34	0.98	1 (3%)
1	A2M	A	2401	1,47	22,25,26	1.46	4 (18%)	31,36,39	2.13	10 (32%)
1	PSU	A	3734	1	18,21,22	1.34	2 (11%)	22,30,33	1.98	4 (18%)
1	PSU	A	4299	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	3637	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.90	3 (13%)
1	PSU	A	3695	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.88	4 (18%)
1	PSU	A	4576	48,1	18,21,22	1.35	2 (11%)	22,30,33	1.85	3 (13%)
1	PSU	A	1860	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	OMG	A	1522	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	OMC	A	2804	1	19,22,23	0.81	0	26,31,34	0.77	0
1	A2M	A	3724	1	22,25,26	1.48	4 (18%)	31,36,39	2.09	8 (25%)
1	OMU	A	4498	48,1	19,22,23	1.20	2 (10%)	26,31,34	1.69	5 (19%)
1	OMU	A	4620	1	19,22,23	1.23	3 (15%)	26,31,34	1.69	4 (15%)
1	PSU	A	3715	1	18,21,22	1.35	2 (11%)	22,30,33	1.87	4 (18%)
1	PSU	A	4420	1	18,21,22	1.40	3 (16%)	22,30,33	1.81	4 (18%)
1	OMG	A	4637	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	OMG	A	4499	1	23,26,27	1.19	3 (13%)	33,38,41	1.94	6 (18%)
1	PSU	A	5001	48,1	18,21,22	1.35	2 (11%)	22,30,33	1.86	3 (13%)
1	PSU	A	4353	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	A2M	A	400	1	22,25,26	1.46	4 (18%)	31,36,39	2.10	10 (32%)
1	PSU	A	4521	48,1,47	18,21,22	1.35	2 (11%)	22,30,33	1.90	3 (13%)
1	A2M	A	3718	1	22,25,26	1.48	4 (18%)	31,36,39	2.05	9 (29%)
1	PSU	A	1536	1	18,21,22	1.35	2 (11%)	22,30,33	1.91	3 (13%)
1	A2M	A	1871	1,47	22,25,26	1.47	4 (18%)	31,36,39	2.09	9 (29%)
1	PSU	A	1677	48,1	18,21,22	1.33	2 (11%)	22,30,33	1.86	3 (13%)
1	OMC	A	2824	1	19,22,23	0.82	0	26,31,34	0.84	0
1	UY1	A	3818	48,1	19,22,23	0.87	0	22,31,34	1.76	4 (18%)
1	OMC	A	1881	1	19,22,23	0.83	0	26,31,34	1.09	2 (7%)
1	OMU	A	4306	1	19,22,23	1.23	3 (15%)	26,31,34	1.70	4 (15%)
1	PSU	A	4500	1	18,21,22	1.37	2 (11%)	22,30,33	1.81	3 (13%)
1	5MC	A	3782	1,47	18,22,23	0.96	2 (11%)	26,32,35	1.16	3 (11%)
1	A2M	A	1323	1	22,25,26	1.48	4 (18%)	31,36,39	2.08	8 (25%)
1	PSU	A	5010	1	18,21,22	1.34	2 (11%)	22,30,33	1.88	3 (13%)
1	OMU	A	3925	1	19,22,23	1.20	2 (10%)	26,31,34	1.69	5 (19%)
1	OMG	A	4623	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	A	4523	1,47	22,25,26	1.46	4 (18%)	31,36,39	2.13	10 (32%)
1	PSU	A	4579	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	OMC	A	2365	1,47	19,22,23	0.81	0	26,31,34	0.79	0
1	PSU	A	1683	48,1	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	4532	1	18,21,22	1.35	2 (11%)	22,30,33	1.88	3 (13%)
1	OMG	A	3944	1	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	PSU	A	4689	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	4972	48,1	18,21,22	1.33	2 (11%)	22,30,33	1.88	3 (13%)
1	PSU	A	1781	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	4 (18%)
1	A2M	A	398	1	22,25,26	1.46	4 (18%)	31,36,39	2.17	10 (32%)
1	PSU	A	1582	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.91	4 (18%)
1	A2M	A	1534	1,47	22,25,26	1.46	4 (18%)	31,36,39	2.09	9 (29%)
1	OMC	A	3701	48,1	19,22,23	0.79	0	26,31,34	0.73	0
1	OMC	A	3869	1	19,22,23	0.82	0	26,31,34	0.86	1 (3%)
1	OMG	A	4392	1	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	OMG	A	3744	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	OMC	A	1340	1	19,22,23	0.83	0	26,31,34	0.88	1 (3%)
1	PSU	A	2508	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	4361	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.86	3 (13%)
1	PSU	A	1792	1	18,21,22	1.34	2 (11%)	22,30,33	1.87	4 (18%)
1	A2M	A	3785	1	22,25,26	1.44	4 (18%)	31,36,39	2.22	11 (35%)
3	PSU	C	55	3	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	1782	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	A2M	A	2787	1,47	22,25,26	1.45	4 (18%)	31,36,39	2.18	9 (29%)
1	OMG	A	2876	1	23,26,27	1.20	3 (13%)	33,38,41	1.97	6 (18%)
1	PSU	A	3768	1	18,21,22	1.35	2 (11%)	22,30,33	1.85	3 (13%)
1	PSU	A	3920	1,47	18,21,22	1.34	2 (11%)	22,30,33	1.91	4 (18%)
1	A2M	A	3867	1	22,25,26	1.47	4 (18%)	31,36,39	2.08	8 (25%)
1	PSU	A	3884	1	18,21,22	1.33	2 (11%)	22,30,33	1.90	3 (13%)
1	OMG	A	2364	1	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	OMG	A	4370	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	PSU	A	4431	48,1	18,21,22	1.35	2 (11%)	22,30,33	1.88	3 (13%)
1	A2M	A	1524	1	22,25,26	1.47	4 (18%)	31,36,39	2.12	8 (25%)
1	OMC	A	2861	1	19,22,23	0.82	0	26,31,34	0.93	1 (3%)
1	OMU	A	2415	1	19,22,23	1.25	4 (21%)	26,31,34	1.71	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	A	3887	1	19,22,23	0.82	0	26,31,34	0.86	1 (3%)
1	OMG	A	4618	48,1	23,26,27	1.19	3 (13%)	33,38,41	1.95	6 (18%)
1	PSU	A	4552	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	A2M	A	4571	1	22,25,26	1.47	4 (18%)	31,36,39	2.10	10 (32%)
1	1MA	A	1322	1,47	21,25,26	1.38	4 (19%)	31,37,40	1.68	5 (16%)
1	OMG	A	4494	1	23,26,27	1.20	3 (13%)	33,38,41	1.96	6 (18%)
1	OMU	A	2837	1	19,22,23	1.24	3 (15%)	26,31,34	1.71	5 (19%)
1	PSU	A	3851	1	18,21,22	1.37	2 (11%)	22,30,33	1.85	4 (18%)
1	PSU	A	3770	1	18,21,22	1.33	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	1744	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	4403	1	18,21,22	1.35	2 (11%)	22,30,33	1.89	4 (18%)
1	5MC	A	4447	48,1	18,22,23	0.99	2 (11%)	26,32,35	1.19	2 (7%)
1	OMU	A	4227	1	19,22,23	1.22	3 (15%)	26,31,34	1.70	4 (15%)
1	OMG	A	3627	1	23,26,27	1.19	3 (13%)	33,38,41	1.95	6 (18%)
1	PSU	A	4312	1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	PSU	A	1862	1	18,21,22	1.34	2 (11%)	22,30,33	1.88	3 (13%)
1	PSU	A	2632	1	18,21,22	1.35	2 (11%)	22,30,33	1.87	3 (13%)
1	PSU	A	4442	1	18,21,22	1.36	2 (11%)	22,30,33	1.90	4 (18%)
1	OMG	A	3899	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	A2M	A	1326	1	22,25,26	1.46	4 (18%)	31,36,39	2.09	8 (25%)
1	OMG	A	2424	1	23,26,27	1.20	3 (13%)	33,38,41	1.91	6 (18%)
1	OMC	A	3841	1	19,22,23	0.80	0	26,31,34	0.78	0
1	PSU	A	4296	1	18,21,22	1.33	2 (11%)	22,30,33	1.93	4 (18%)
1	OMG	A	1625	48,1	23,26,27	1.20	3 (13%)	33,38,41	1.94	6 (18%)
1	OMC	A	4536	1,47	19,22,23	0.84	0	26,31,34	0.97	1 (3%)
1	OMG	A	4196	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	PSU	A	4293	1	18,21,22	1.34	2 (11%)	22,30,33	1.88	3 (13%)
1	PSU	A	4457	1	18,21,22	1.34	2 (11%)	22,30,33	1.88	4 (18%)
1	A2M	A	3830	1	22,25,26	1.47	4 (18%)	31,36,39	2.10	10 (32%)
1	PSU	A	4471	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.90	4 (18%)
1	A2M	A	2363	1,47	22,25,26	1.47	4 (18%)	31,36,39	2.11	9 (29%)
3	OMG	C	75	3	23,26,27	1.21	3 (13%)	33,38,41	1.94	6 (18%)
1	6MZ	A	4220	1	22,25,26	1.43	4 (18%)	30,36,39	2.18	9 (30%)
1	PSU	A	3639	1	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
1	OMG	A	4228	1	23,26,27	1.18	3 (13%)	33,38,41	1.93	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMC	A	2351	1,47	19,22,23	0.82	0	26,31,34	0.87	1 (3%)
1	PSU	A	3730	1	18,21,22	1.33	2 (11%)	22,30,33	1.87	3 (13%)
1	OMC	A	3808	48,1	19,22,23	0.83	0	26,31,34	0.94	1 (3%)
1	PSU	A	4493	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.89	4 (18%)
3	PSU	C	69	3	18,21,22	1.35	2 (11%)	22,30,33	1.88	4 (18%)
1	A2M	A	2815	48,1	22,25,26	1.47	4 (18%)	31,36,39	2.12	8 (25%)
1	OMG	A	1316	48,1	23,26,27	1.21	3 (13%)	33,38,41	1.95	6 (18%)
1	PSU	A	2839	1	18,21,22	1.33	2 (11%)	22,30,33	1.87	3 (13%)
1	PSU	A	4423	1	18,21,22	1.35	2 (11%)	22,30,33	1.88	3 (13%)
1	PSU	A	3853	1,47	18,21,22	1.36	2 (11%)	22,30,33	1.87	3 (13%)
1	OMG	A	3792	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	A2M	A	3825	1	22,25,26	1.48	4 (18%)	31,36,39	2.07	8 (25%)
1	UR3	A	4530	1	19,22,23	1.00	1 (5%)	26,32,35	1.41	1 (3%)
1	PSU	A	4628	1	18,21,22	1.35	2 (11%)	22,30,33	1.89	3 (13%)
1	OMC	A	2422	1,47	19,22,23	0.82	0	26,31,34	0.84	1 (3%)
1	PSU	A	4673	48,1	18,21,22	1.34	2 (11%)	22,30,33	1.89	3 (13%)
1	A2M	A	4590	1	22,25,26	1.47	4 (18%)	31,36,39	2.09	8 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	3844	1	-	1/7/25/26	0/2/2/2
1	OMC	A	4456	1	-	2/9/27/28	0/2/2/2
1	A2M	A	2401	1,47	-	0/9/27/28	0/3/3/3
1	PSU	A	3734	1	-	4/7/25/26	0/2/2/2
1	PSU	A	4299	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3637	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	3695	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4576	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1860	1	-	0/7/25/26	0/2/2/2
1	OMG	A	1522	1	-	0/9/27/28	0/3/3/3
1	OMC	A	2804	1	-	0/9/27/28	0/2/2/2
1	A2M	A	3724	1	-	0/9/27/28	0/3/3/3
1	OMU	A	4498	48,1	-	0/9/27/28	0/2/2/2
1	OMU	A	4620	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	3715	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4420	1	-	3/7/25/26	0/2/2/2
1	OMG	A	4637	1	-	0/9/27/28	0/3/3/3
1	OMG	A	4499	1	-	0/9/27/28	0/3/3/3
1	PSU	A	5001	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4353	48,1	-	0/7/25/26	0/2/2/2
1	A2M	A	400	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4521	48,1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	3718	1	-	0/9/27/28	0/3/3/3
1	PSU	A	1536	1	-	0/7/25/26	0/2/2/2
1	A2M	A	1871	1,47	-	0/9/27/28	0/3/3/3
1	PSU	A	1677	48,1	-	4/7/25/26	0/2/2/2
1	OMC	A	2824	1	-	2/9/27/28	0/2/2/2
1	UY1	A	3818	48,1	-	5/9/27/28	0/2/2/2
1	OMC	A	1881	1	-	5/9/27/28	0/2/2/2
1	OMU	A	4306	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4500	1	-	2/7/25/26	0/2/2/2
1	5MC	A	3782	1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	1323	1	-	0/9/27/28	0/3/3/3
1	PSU	A	5010	1	-	0/7/25/26	0/2/2/2
1	OMU	A	3925	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4623	1	-	0/9/27/28	0/3/3/3
1	A2M	A	4523	1,47	-	2/9/27/28	0/3/3/3
1	PSU	A	4579	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2365	1,47	-	0/9/27/28	0/2/2/2
1	PSU	A	1683	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4532	1	-	0/7/25/26	0/2/2/2
1	OMG	A	3944	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4689	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4972	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1781	1	-	0/7/25/26	0/2/2/2
1	A2M	A	398	1	-	2/9/27/28	0/3/3/3
1	PSU	A	1582	48,1	-	0/7/25/26	0/2/2/2
1	A2M	A	1534	1,47	-	2/9/27/28	0/3/3/3
1	OMC	A	3701	48,1	-	5/9/27/28	0/2/2/2
1	OMC	A	3869	1	-	0/9/27/28	0/2/2/2
1	OMG	A	4392	1	-	0/9/27/28	0/3/3/3
1	OMG	A	3744	1	-	0/9/27/28	0/3/3/3
1	OMC	A	1340	1	-	0/9/27/28	0/2/2/2
1	PSU	A	2508	1	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	A	4361	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	1792	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3785	1	-	2/9/27/28	0/3/3/3
3	PSU	C	55	3	-	0/7/25/26	0/2/2/2
1	PSU	A	1782	1	-	0/7/25/26	0/2/2/2
1	A2M	A	2787	1,47	-	3/9/27/28	0/3/3/3
1	OMG	A	2876	1	-	1/9/27/28	0/3/3/3
1	PSU	A	3768	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3920	1,47	-	0/7/25/26	0/2/2/2
1	A2M	A	3867	1	-	1/9/27/28	0/3/3/3
1	PSU	A	3884	1	-	0/7/25/26	0/2/2/2
1	OMG	A	2364	1	-	2/9/27/28	0/3/3/3
1	OMG	A	4370	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4431	48,1	-	0/7/25/26	0/2/2/2
1	A2M	A	1524	1	-	0/9/27/28	0/3/3/3
1	OMC	A	2861	1	-	1/9/27/28	0/2/2/2
1	OMU	A	2415	1	-	2/9/27/28	0/2/2/2
1	OMC	A	3887	1	-	2/9/27/28	0/2/2/2
1	OMG	A	4618	48,1	-	0/9/27/28	0/3/3/3
1	PSU	A	4552	1	-	0/7/25/26	0/2/2/2
1	A2M	A	4571	1	-	1/9/27/28	0/3/3/3
1	1MA	A	1322	1,47	-	0/7/25/26	0/3/3/3
1	OMG	A	4494	1	-	0/9/27/28	0/3/3/3
1	OMU	A	2837	1	-	0/9/27/28	0/2/2/2
1	PSU	A	3851	1	-	1/7/25/26	0/2/2/2
1	PSU	A	3770	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1744	48,1	-	0/7/25/26	0/2/2/2
1	PSU	A	4403	1	-	0/7/25/26	0/2/2/2
1	5MC	A	4447	48,1	-	4/7/25/26	0/2/2/2
1	OMU	A	4227	1	-	0/9/27/28	0/2/2/2
1	OMG	A	3627	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4312	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1862	1	-	0/7/25/26	0/2/2/2
1	PSU	A	2632	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4442	1	-	0/7/25/26	0/2/2/2
1	OMG	A	3899	1	-	0/9/27/28	0/3/3/3
1	A2M	A	1326	1	-	1/9/27/28	0/3/3/3
1	OMG	A	2424	1	-	0/9/27/28	0/3/3/3
1	OMC	A	3841	1	-	0/9/27/28	0/2/2/2
1	PSU	A	4296	1	-	0/7/25/26	0/2/2/2
1	OMG	A	1625	48,1	-	1/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	A	4536	1,47	-	3/9/27/28	0/2/2/2
1	OMG	A	4196	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4293	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4457	1	-	0/7/25/26	0/2/2/2
1	A2M	A	3830	1	-	0/9/27/28	0/3/3/3
1	PSU	A	4471	48,1	-	0/7/25/26	0/2/2/2
1	A2M	A	2363	1,47	-	0/9/27/28	0/3/3/3
3	OMG	C	75	3	-	0/9/27/28	0/3/3/3
1	6MZ	A	4220	1	-	0/9/27/28	0/3/3/3
1	PSU	A	3639	1	-	0/7/25/26	0/2/2/2
1	OMG	A	4228	1	-	0/9/27/28	0/3/3/3
1	OMC	A	2351	1,47	-	1/9/27/28	0/2/2/2
1	PSU	A	3730	1	-	0/7/25/26	0/2/2/2
1	OMC	A	3808	48,1	-	0/9/27/28	0/2/2/2
1	PSU	A	4493	48,1	-	0/7/25/26	0/2/2/2
3	PSU	C	69	3	-	0/7/25/26	0/2/2/2
1	A2M	A	2815	48,1	-	0/9/27/28	0/3/3/3
1	OMG	A	1316	48,1	-	0/9/27/28	0/3/3/3
1	PSU	A	2839	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4423	1	-	0/7/25/26	0/2/2/2
1	PSU	A	3853	1,47	-	0/7/25/26	0/2/2/2
1	OMG	A	3792	1	-	0/9/27/28	0/3/3/3
1	A2M	A	3825	1	-	0/9/27/28	0/3/3/3
1	UR3	A	4530	1	-	0/7/25/26	0/2/2/2
1	PSU	A	4628	1	-	0/7/25/26	0/2/2/2
1	OMC	A	2422	1,47	-	0/9/27/28	0/2/2/2
1	PSU	A	4673	48,1	-	0/7/25/26	0/2/2/2
1	A2M	A	4590	1	-	1/9/27/28	0/3/3/3

The worst 5 of 285 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3718	A2M	C5-C4	4.57	1.47	1.39
1	A	3724	A2M	C5-C4	4.56	1.47	1.39
1	A	2815	A2M	C5-C4	4.55	1.47	1.39
1	A	1524	A2M	C5-C4	4.55	1.47	1.39
1	A	3825	A2M	C5-C4	4.54	1.47	1.39

The worst 5 of 551 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2815	A2M	C5-C4-N3	-6.51	118.25	126.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3724	A2M	C5-C4-N3	-6.43	118.36	126.75
1	A	1524	A2M	C5-C4-N3	-6.41	118.39	126.75
1	A	2876	OMG	C5-C4-N3	-6.35	118.16	128.46
1	A	3825	A2M	C5-C4-N3	-6.33	118.49	126.75

There are no chirality outliers.

5 of 66 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1326	A2M	C1'-C2'-O2'-CM'
1	A	1677	PSU	C2'-C1'-C5-C4
1	A	1881	OMC	O4'-C1'-N1-C2
1	A	1881	OMC	O4'-C1'-N1-C6
1	A	1881	OMC	C3'-C4'-C5'-O5'

There are no ring outliers.

65 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	4456	OMC	1	0
1	A	3734	PSU	1	0
1	A	4299	PSU	1	0
1	A	4576	PSU	1	0
1	A	2804	OMC	3	0
1	A	3724	A2M	2	0
1	A	4620	OMU	2	0
1	A	3715	PSU	1	0
1	A	4420	PSU	2	0
1	A	4637	OMG	1	0
1	A	4353	PSU	1	0
1	A	3718	A2M	3	0
1	A	1871	A2M	1	0
1	A	1677	PSU	1	0
1	A	3818	UY1	1	0
1	A	1881	OMC	1	0
1	A	4306	OMU	1	0
1	A	4500	PSU	1	0
1	A	3925	OMU	1	0
1	A	4623	OMG	1	0
1	A	4523	A2M	2	0
1	A	4579	PSU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1683	PSU	2	0
1	A	3944	OMG	2	0
1	A	4689	PSU	1	0
1	A	398	A2M	1	0
1	A	3869	OMC	1	0
1	A	4392	OMG	2	0
1	A	1340	OMC	2	0
1	A	3785	A2M	1	0
1	A	2876	OMG	1	0
1	A	3867	A2M	2	0
1	A	3884	PSU	2	0
1	A	2364	OMG	1	0
1	A	1524	A2M	1	0
1	A	2861	OMC	1	0
1	A	2415	OMU	1	0
1	A	3887	OMC	1	0
1	A	4618	OMG	2	0
1	A	4552	PSU	2	0
1	A	4571	A2M	1	0
1	A	2837	OMU	1	0
1	A	3770	PSU	1	0
1	A	4403	PSU	1	0
1	A	4447	5MC	1	0
1	A	4227	OMU	1	0
1	A	1326	A2M	3	0
1	A	4536	OMC	2	0
1	A	4196	OMG	1	0
1	A	4293	PSU	1	0
1	A	4457	PSU	2	0
1	A	3830	A2M	2	0
1	A	4471	PSU	2	0
1	A	2363	A2M	2	0
3	C	75	OMG	2	0
1	A	4220	6MZ	2	0
1	A	2351	OMC	1	0
1	A	3808	OMC	1	0
3	C	69	PSU	1	0
1	A	2815	A2M	1	0
1	A	1316	OMG	2	0
1	A	2839	PSU	1	0
1	A	3792	OMG	1	0
1	A	3825	A2M	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	4590	A2M	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 391 ligands modelled in this entry, 389 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	GTP	B	205	2	30,34,34	0.50	0	46,54,54	0.53	0
51	EPE	M	201	-	15,15,15	0.81	1 (6%)	18,20,20	1.73	6 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	B	205	2	-	0/22/38/38	0/3/3/3
51	EPE	M	201	-	-	5/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	M	201	EPE	C10-S	2.74	1.81	1.77

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	M	201	EPE	C5-N4-C3	4.20	118.28	108.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	M	201	EPE	C7-N4-C3	2.74	118.23	111.23
51	M	201	EPE	C7-N4-C5	2.63	117.96	111.23
51	M	201	EPE	O3S-S-C10	2.33	109.53	105.77
51	M	201	EPE	O2S-S-C10	2.20	109.56	106.92

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
51	M	201	EPE	C10-C9-N1-C2
51	M	201	EPE	C9-C10-S-O1S
51	M	201	EPE	C9-C10-S-O3S
51	M	201	EPE	C9-C10-S-O2S
51	M	201	EPE	C8-C7-N4-C5

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
50	B	205	GTP	1	0
51	M	201	EPE	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

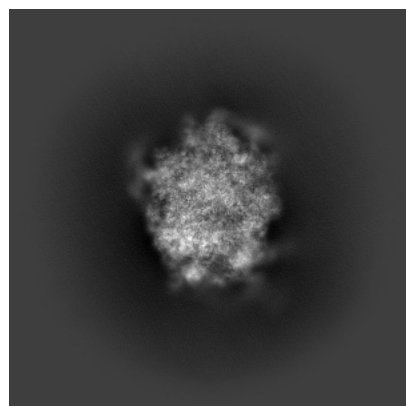
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51452. These allow visual inspection of the internal detail of the map and identification of artifacts.

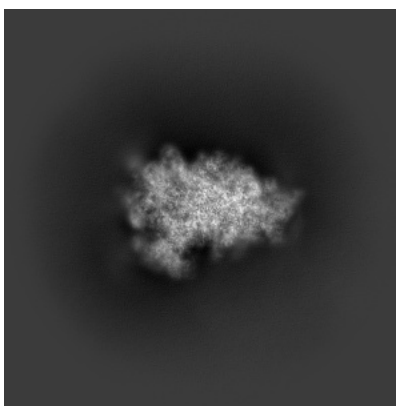
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

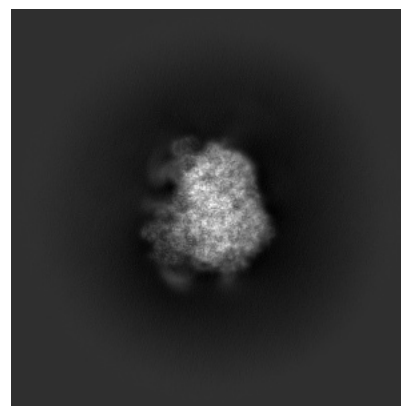
6.1.1 Primary map



X

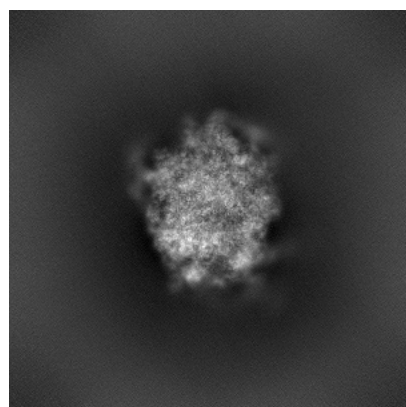


Y

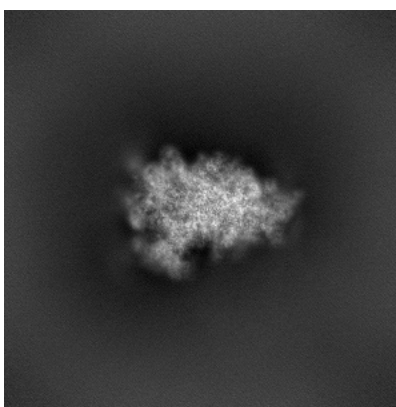


Z

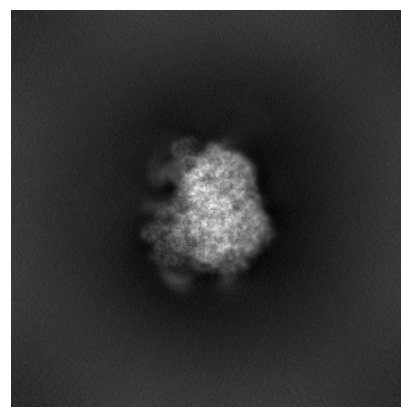
6.1.2 Raw map



X



Y

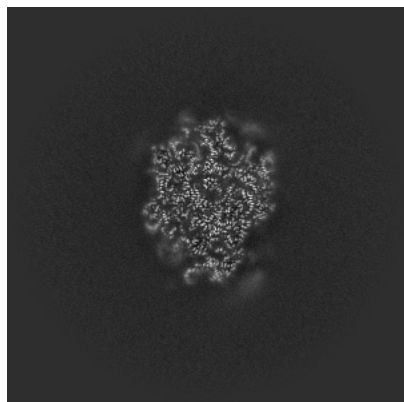


Z

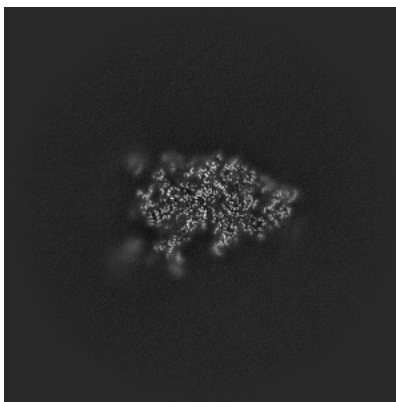
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

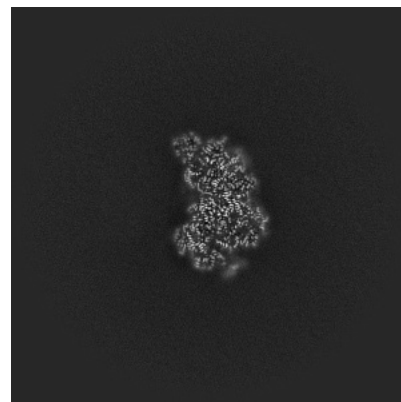
6.2.1 Primary map



X Index: 280

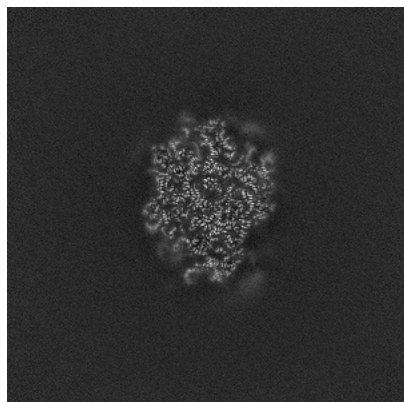


Y Index: 280

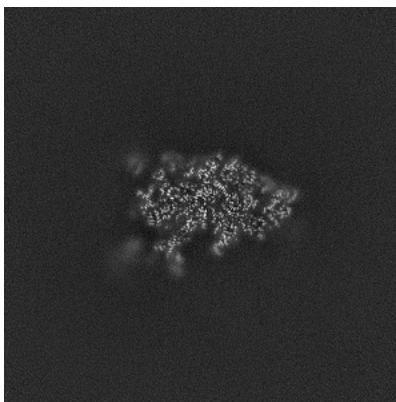


Z Index: 280

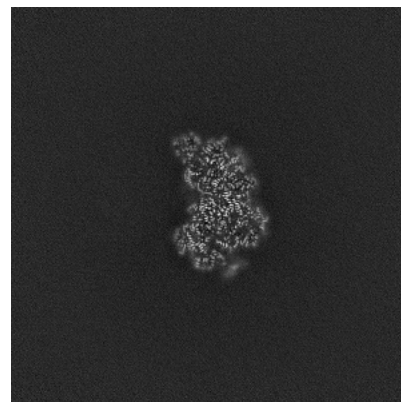
6.2.2 Raw map



X Index: 280



Y Index: 280

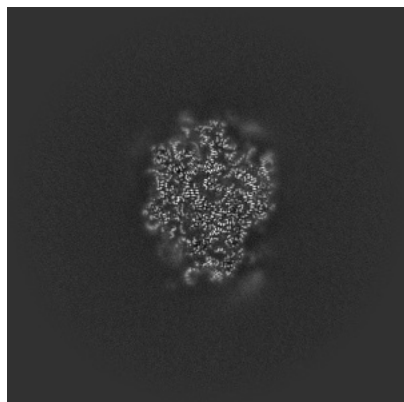


Z Index: 280

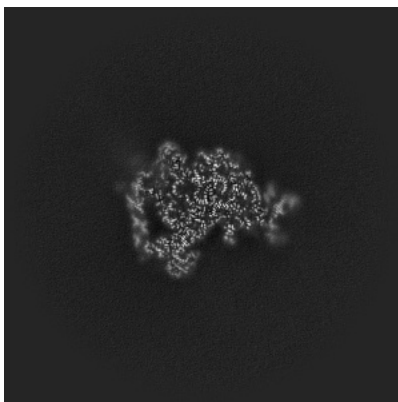
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

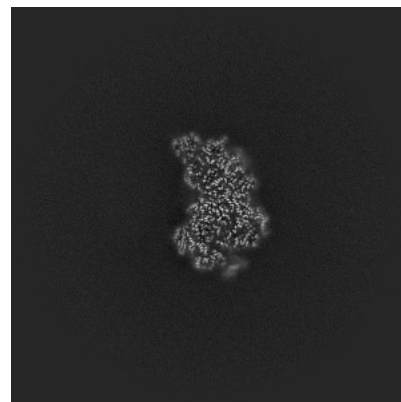
6.3.1 Primary map



X Index: 281

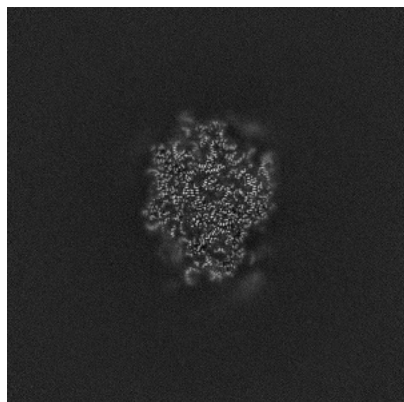


Y Index: 252

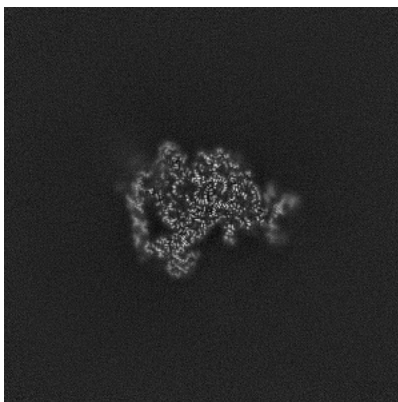


Z Index: 279

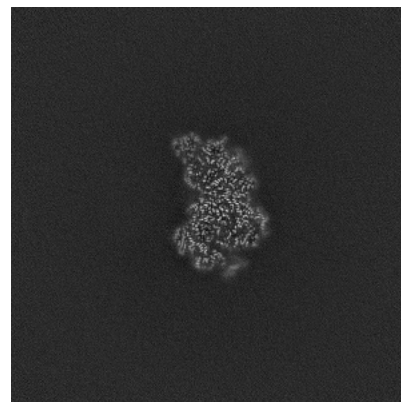
6.3.2 Raw map



X Index: 282



Y Index: 252

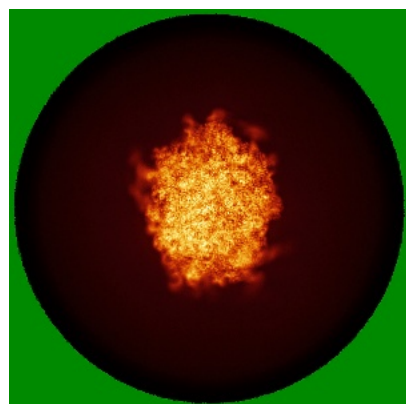


Z Index: 279

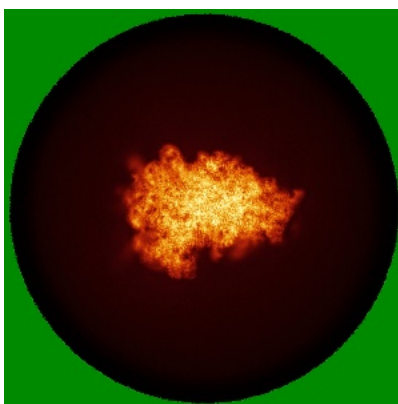
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

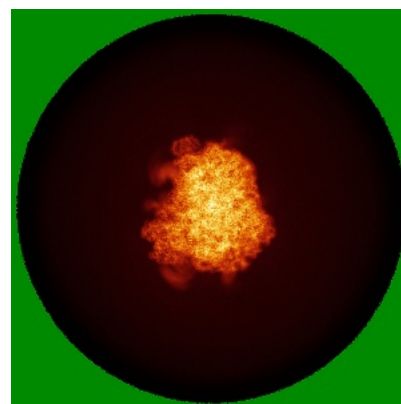
6.4.1 Primary map



X

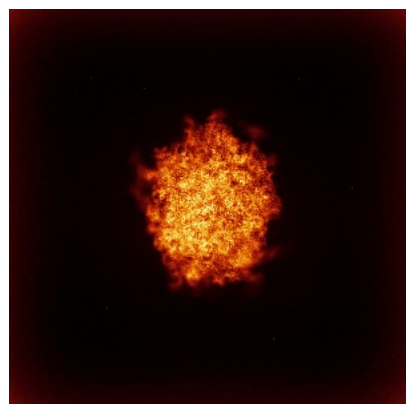


Y

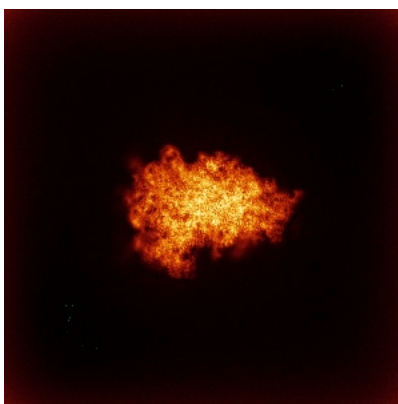


Z

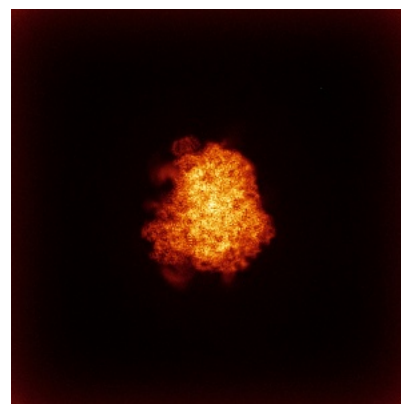
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

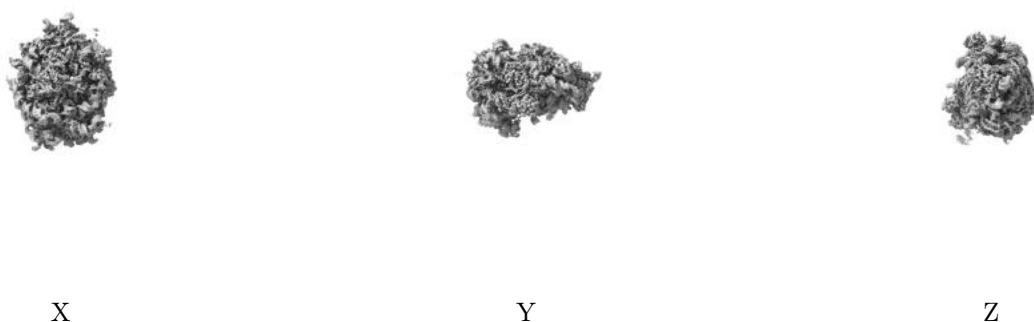
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

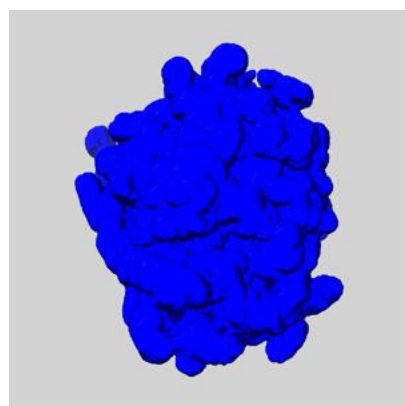
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

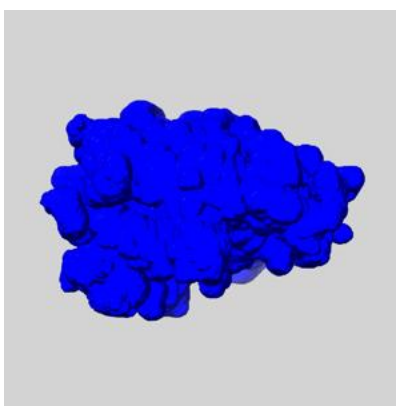
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

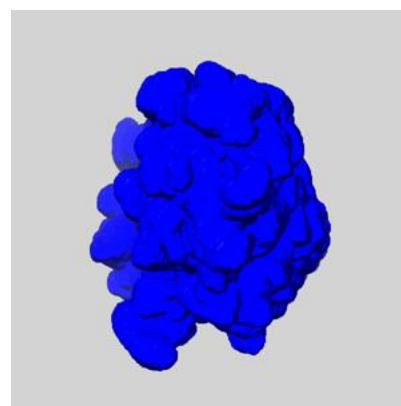
6.6.1 emd_51452_msk_1.map [i](#)



X



Y

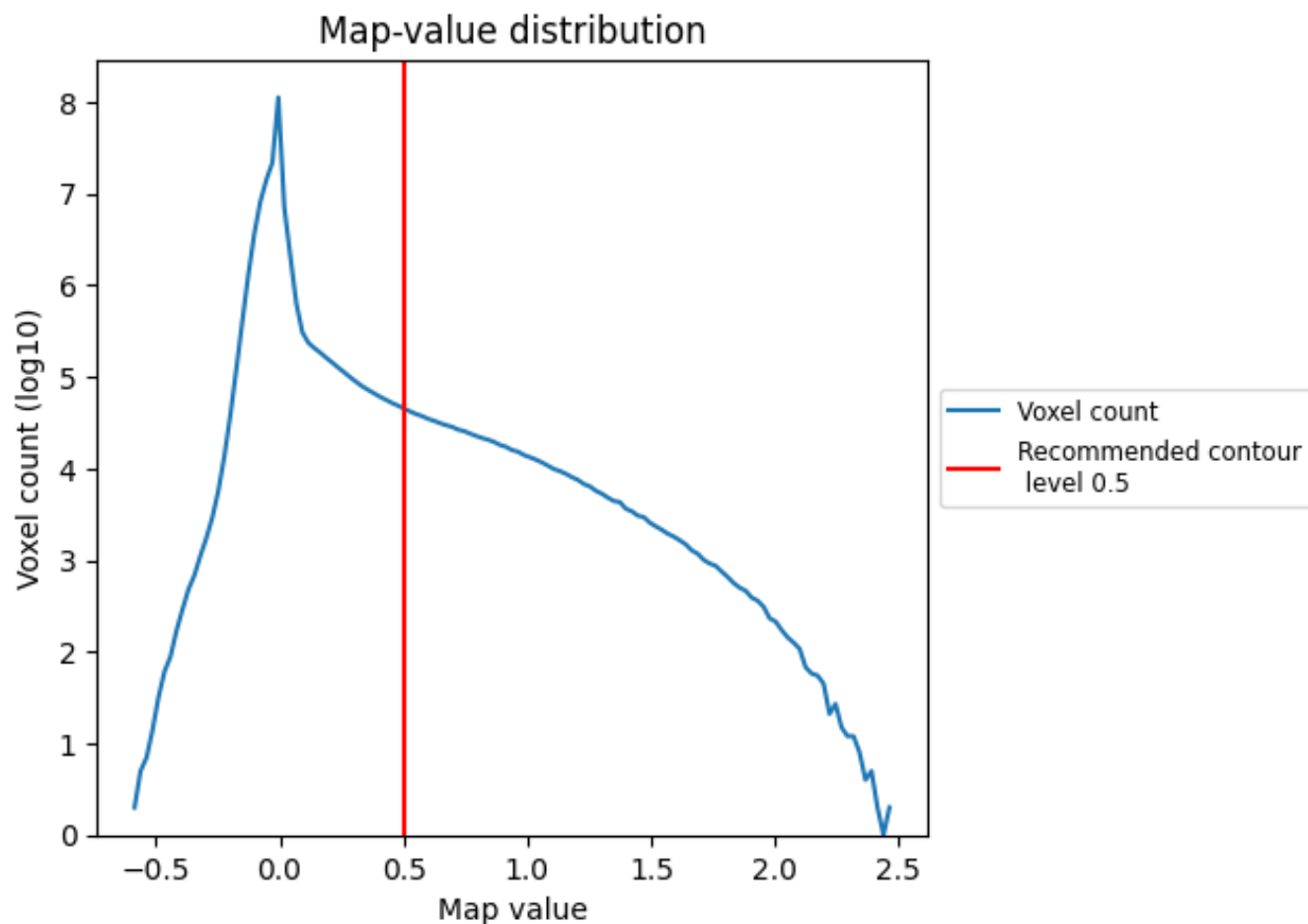


Z

7 Map analysis [i](#)

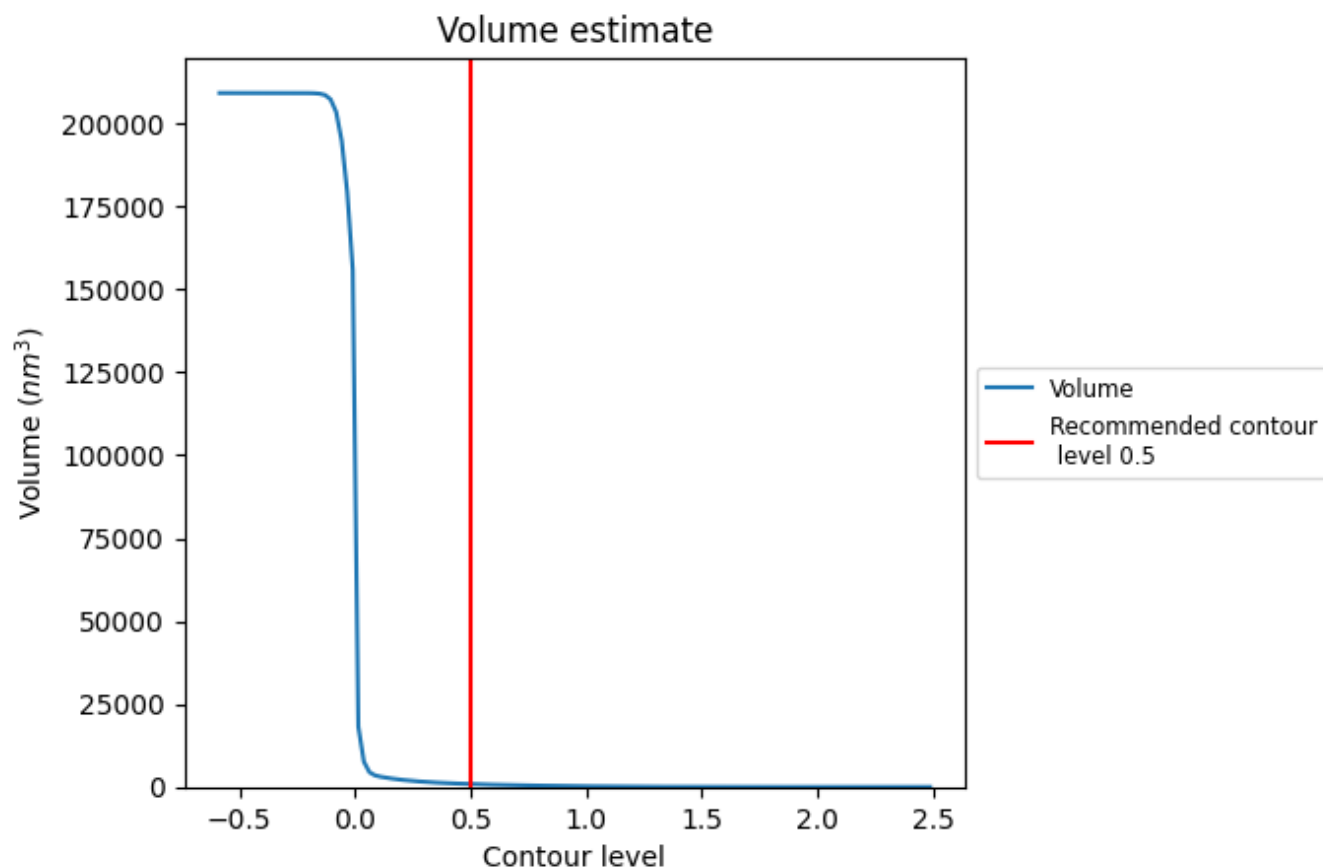
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

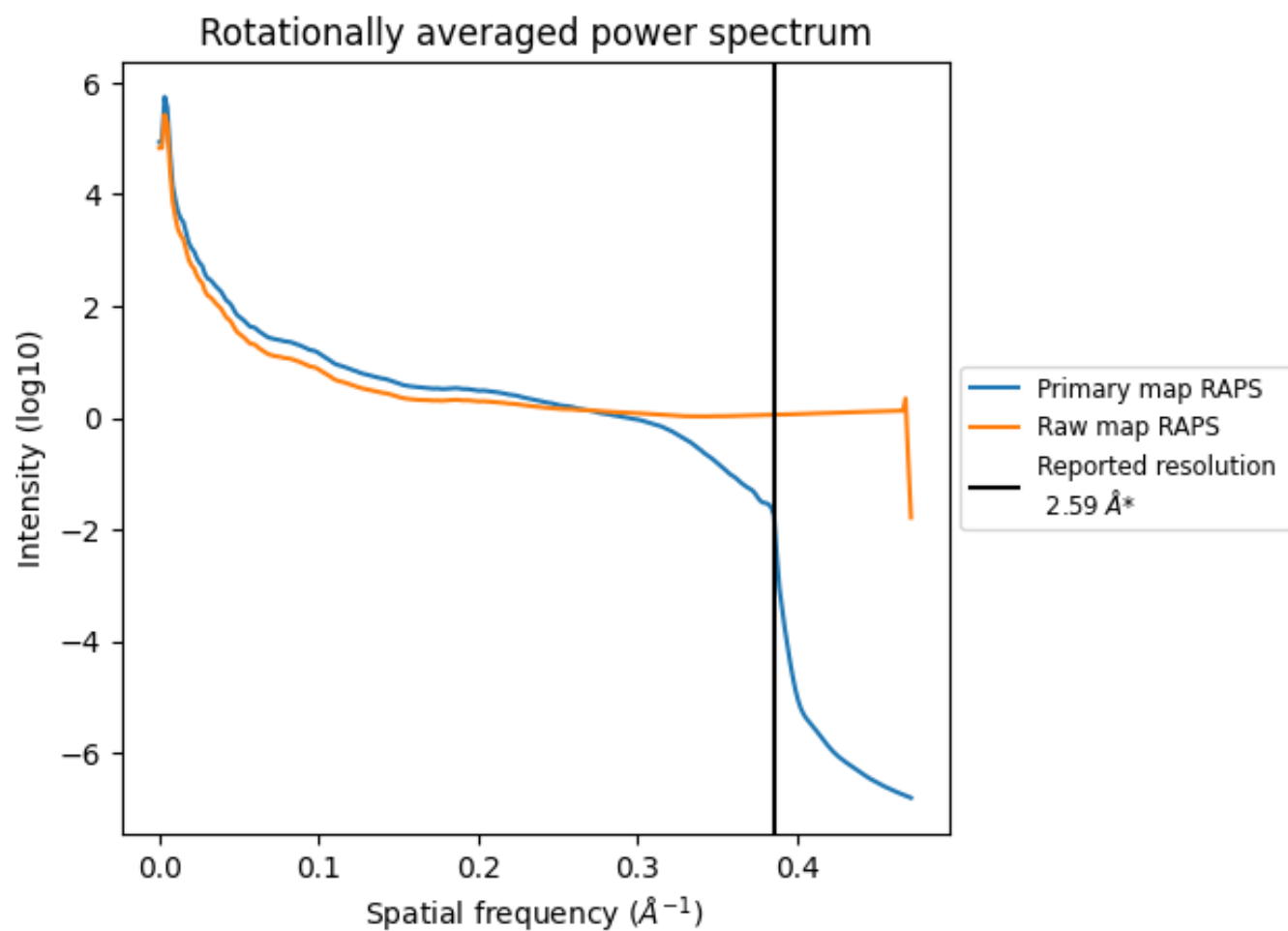
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 877 nm^3 ; this corresponds to an approximate mass of 792 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

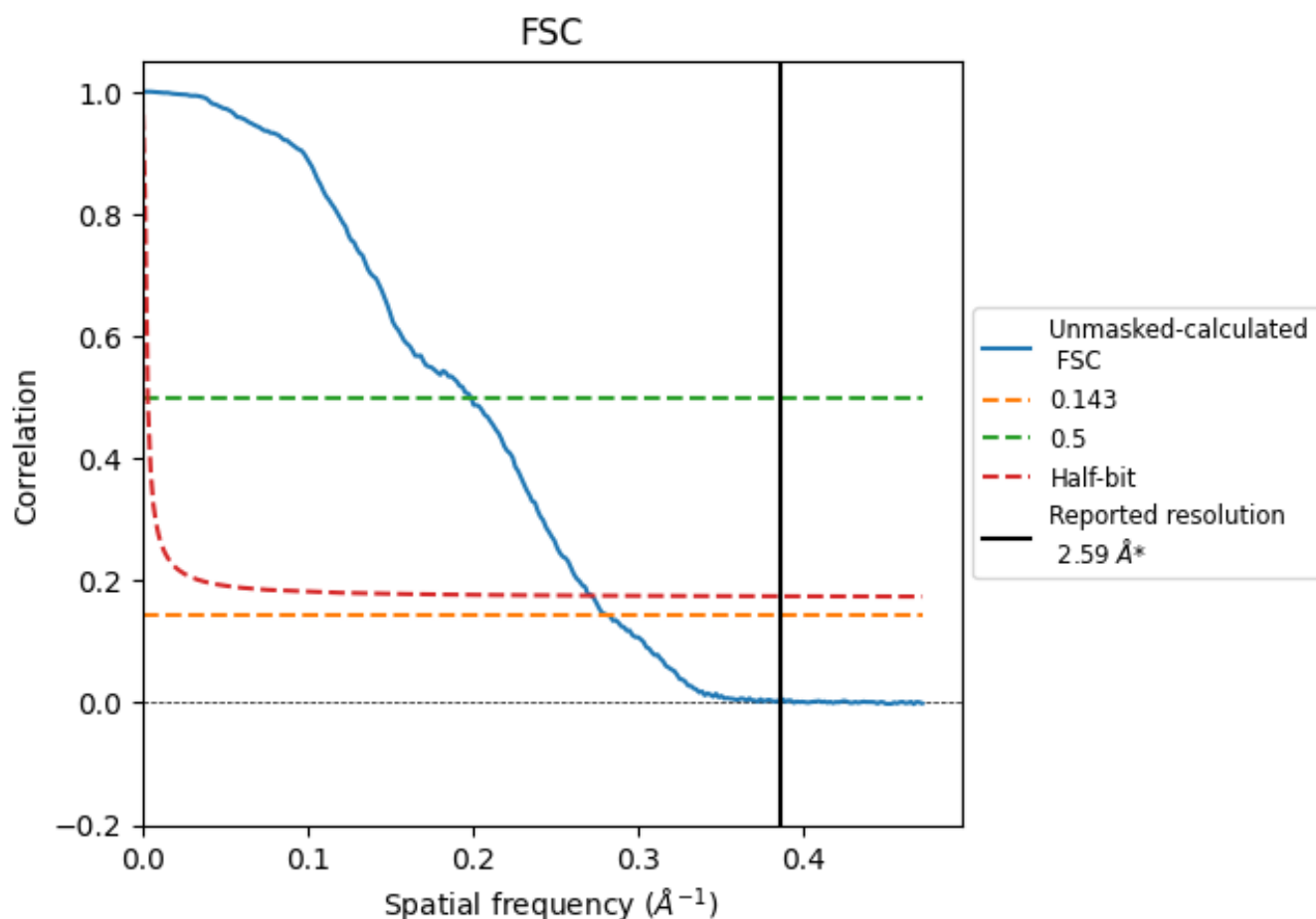


*Reported resolution corresponds to spatial frequency of $0.386 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.386 Å⁻¹

8.2 Resolution estimates [i](#)

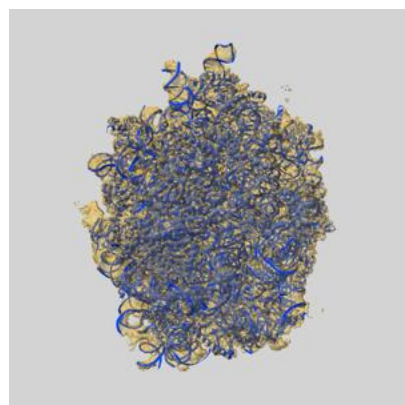
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.59	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.55	5.03	3.68

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.55 differs from the reported value 2.59 by more than 10 %

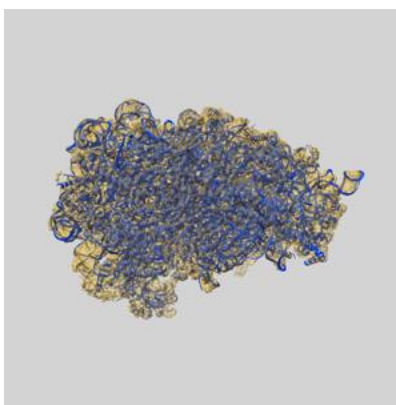
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51452 and PDB model 9GMO. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

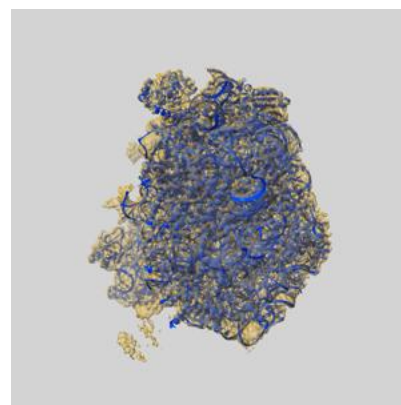
9.1 Map-model overlay [i](#)



X



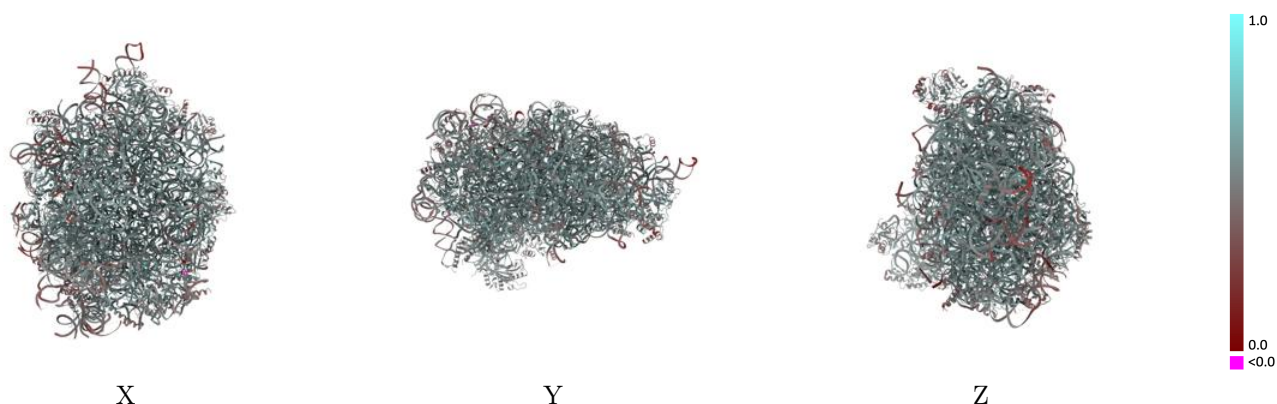
Y



Z

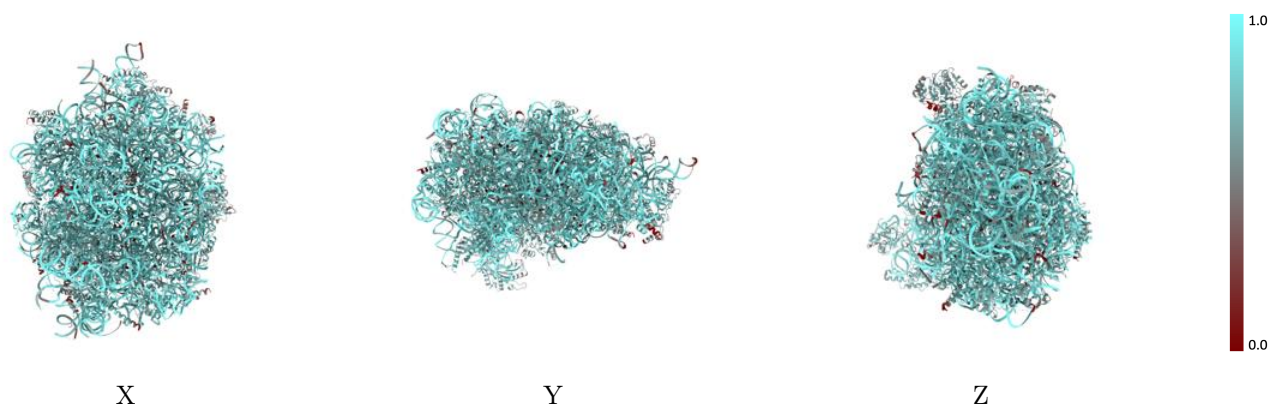
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



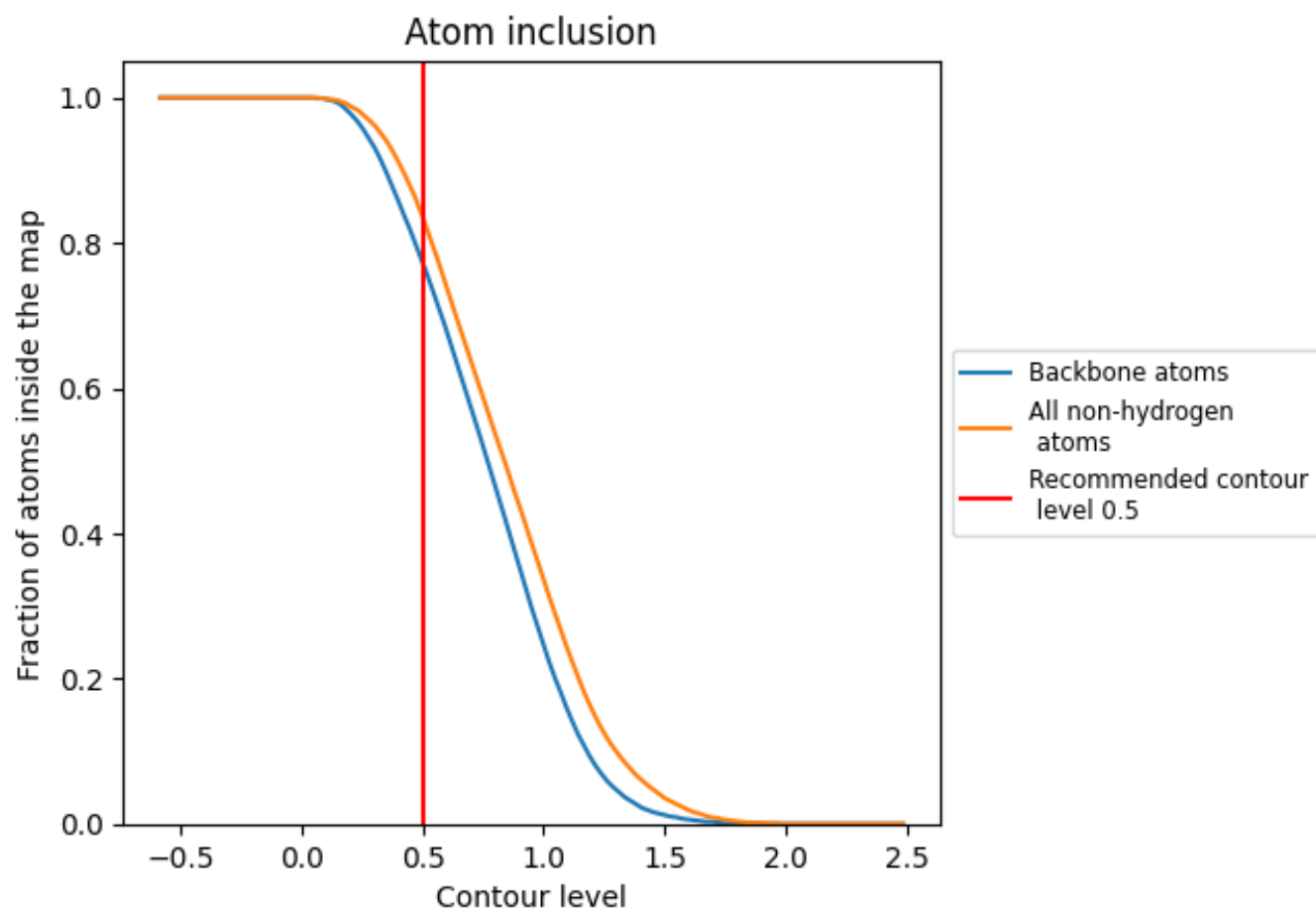
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8350	 0.5360
0	 0.1820	 0.4420
A	 0.9040	 0.5330
B	 0.9550	 0.5510
C	 0.9280	 0.5480
D	 0.7890	 0.5740
E	 0.7780	 0.5540
F	 0.7800	 0.5590
G	 0.7650	 0.5170
H	 0.7490	 0.5260
I	 0.7740	 0.5560
J	 0.7930	 0.5540
K	 0.7670	 0.5670
L	 0.7590	 0.5250
M	 0.7870	 0.5620
N	 0.7480	 0.5390
O	 0.6480	 0.4540
P	 0.7450	 0.5570
Q	 0.7260	 0.5410
R	 0.7620	 0.5430
S	 0.7790	 0.5420
T	 0.7160	 0.5190
U	 0.8070	 0.5700
V	 0.6970	 0.5170
W	 0.6460	 0.4960
X	 0.7500	 0.5460
Y	 0.7790	 0.5700
Z	 0.8230	 0.5860
a	 0.7200	 0.5470
b	 0.7530	 0.5200
c	 0.7030	 0.5030
d	 0.8290	 0.5770
e	 0.6300	 0.4860
f	 0.7550	 0.5690
g	 0.7670	 0.5460



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Chain	Atom inclusion	Q-score
h	 0.5910	 0.4670
i	 0.7010	 0.5510
j	 0.7040	 0.5300
k	 0.8100	 0.5620
l	 0.8260	 0.5830
m	 0.7680	 0.5520
n	 0.7030	 0.5060
o	 0.7300	 0.5290
p	 0.7540	 0.5430
q	 0.6960	 0.4860
r	 0.7390	 0.5340
s	 0.7860	 0.5300